

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 17, 2006, 01:25:09 ; Search time 47 Seconds

(without alignments)
561.139 Million cell updates/sec

Title: US-10-634-027-7

Perfect score: 1744

Sequence: 1 GRLPSVHLNLCQKGNKRTS.....VDVLRARLRKLRSEHHHH 319

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:

1: /cgn2_6/prodata/1/aa/5/COMB.pep:*

2: /cgn2_6/prodata/1/aa/6/COMB.pep:*

3: /cgn2_6/prodata/1/aa/H/COMB.pep:*

4: /cgn2_6/prodata/1/aa/PCTUS/COMB.pep:*

5: /cgn2_6/prodata/1/aa/R/COMB.pep:*

6: /cgn2_6/prodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1691	97.0	1997	2	US-09-949-016-6275 Sequence 6275, Ap
2	1644	94.3	1907	2	US-09-949-016-8045 Sequence 8045, Ap
3	1444	82.8	278	1	US-08-201-697-16 Sequence 16, Appl
4	1374	78.8	254	1	US-08-685-925-14 Sequence 14, Appl
5	1374	78.8	254	1	US-09-144-925-14 Sequence 14, Appl
6	878.5	50.4	1337	2	US-08-854-585-2 Sequence 2, Appl1
7	878.5	50.4	1337	2	US-09-447-533-2 Sequence 2, Appl1
8	878.5	50.4	1337	4	PCT-US95-05512-2 Sequence 17, Appl
9	843.5	48.4	273	1	US-08-201-697-17 Sequence 17, Appl
10	765	43.9	506	2	US-09-949-016-8833 Sequence 8833, Ap
11	765	43.9	506	2	US-09-949-016-8834 Sequence 8834, Ap
12	765	43.9	506	2	US-09-949-016-8835 Sequence 8835, Ap
13	765	43.9	506	2	US-09-949-016-8836 Sequence 8836, Ap
14	765	43.9	506	2	US-09-949-016-8837 Sequence 8837, Ap
15	765	43.9	506	2	US-09-949-016-8838 Sequence 8838, Ap
16	765	43.9	1274	2	US-09-949-016-8828 Sequence 8828, Ap
17	765	43.9	1274	2	US-09-949-016-8829 Sequence 8829, Ap
18	765	43.9	1274	2	US-09-949-016-8830 Sequence 8830, Ap
19	765	43.9	1274	2	US-09-949-016-8831 Sequence 8831, Ap
20	765	43.9	1274	2	US-09-949-016-8832 Sequence 8832, Ap
21	761.5	43.7	1246	1	US-08-201-697-4 Sequence 4, Appl
22	761.5	43.7	1246	1	US-08-201-697-4 Sequence 4, Appl
23	761.5	43.7	1246	2	US-09-949-016-8051 Sequence 8051, Ap
24	761.5	43.7	1246	2	US-09-949-016-8052 Sequence 8052, Ap
25	761.5	43.7	1246	2	US-09-949-016-8053 Sequence 8053, Ap
26	761.5	43.7	1246	2	US-09-949-016-8054 Sequence 8054, Ap
27	760.5	43.6	1187	1	US-08-201-697-2 Sequence 2, Appl1

28	744.5	42.7	251	1	US-08-685-992-15	Sequence 15, Appl
29	744.5	42.7	251	1	US-09-144-925-15	Sequence 15, Appl
30	697.5	40.0	1711	1	US-08-343-930-2	Sequence 2, Appl1
31	675	38.7	2301	2	US-09-822-871-4	Sequence 4, Appl
32	673	38.6	401	2	US-09-361-096A-15	Sequence 15, Appl
33	673	38.6	402	1	US-08-036-609-15	Sequence 15, Appl
34	673	38.6	402	1	US-08-036-609-15	Sequence 15, Appl
35	673	38.6	898	1	US-08-036-210-22	Sequence 22, Appl
36	673	38.6	898	1	US-08-036-210-22	Sequence 22, Appl
37	673	38.6	898	1	US-08-036-210-22	Sequence 22, Appl
38	667	38.2	289	2	US-09-361-096A-22	Sequence 22, Appl
39	667	38.2	322	1	US-08-036-210-11	Sequence 11, Appl
40	667	38.2	322	1	US-08-036-210-11	Sequence 11, Appl
41	667	38.2	322	2	US-09-361-096A-11	Sequence 11, Appl
42	658	37.7	2291	2	US-09-822-871-2	Sequence 2, Appl1
43	643.5	36.9	255	1	US-08-685-992-16	Sequence 16, Appl
44	643.5	36.9	255	1	US-09-144-925-16	Sequence 16, Appl
45	618.5	35.5	2314	2	US-09-816-703A-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1	US-09-949-016-6275	Sequence 6275, Application US/09949016
Patent No. 6812339		
GENERAL INFORMATION:		
APPLICANT: VENTNER, J. Craig et al.		
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASES, METHODS OF DETECTION AND USES THEREOF		
FILE REFERENCE: CL001037		
CURRENT APPLICATION NUMBER: US/09/949, 016		
PRIOR FILING DATE: 2000-04-14		
PRIOR APPLICATION NUMBER: 60/241, 755		
PRIOR FILING DATE: 2000-10-20		
PRIOR APPLICATION NUMBER: 60/237, 768		
PRIOR FILING DATE: 2000-10-03		
PRIOR APPLICATION NUMBER: 60/231, 498		
PRIOR FILING DATE: 2000-09-08		
NUMBER OF SEQ ID NOS: 207012		
SOFTWARE: FASTSEQ for Windows Version 4.0		
SEQ ID NO 6275		
LENGTH: 1997		
TYPE: PMT		
ORGANISM: Human		
US-09-949-016-6275		
Query Match	97.0%	Score 1691; DB 2; Length 1997;
Best Local Similarity	99.4%	Pred. No. 8.1e-170;
Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		
QY	2	DRLPSVHLNLCQKGNKRTSCTPKINQFBGFMKLDQNSVILSKTEYBEIKVYGRNOSCDI 61
DB	1662	DRLPSVHLNLCQKGNKRTSCTPKINQFBGFMKLDQNSVILSKTEYBEIKVYGRNOSCDI 1721
QY	62	ALLPENRGNRYNNILPYDATVVKLSVNDPCSDYINASYIPNNFREYVLTGGLPG 121
DB	1722	ALLPENRGNRYNNILPYDATVVKLSVNDPCSDYINASYIPNNFREYVLTGGLPG 1781
QY	122	TKDDFWKVMQYNNIIVAVTQCVKGRVACDHWYPADODSLYYGDLIIQMLSESVLEW 181
DB	1782	TKDDFWKVMQYNNIIVAVTQCVKGRVACDHWYPADODSLYYGDLIIQMLSESVLEW 1841
QY	182	TIREPFTGSEGLDARHLIRHRYTWPDHGVPEPTTOSLIQFVATVDYINNSPQAPTV 241
DB	1842	TIREPFTGSEGLDARHLIRHRYTWPDHGVPEPTTOSLIQFVATVDYINNSPQAPTV 1901
QY	242	VHCSAGVGRGTFTALDRILQDLSKDSVDIYGAVHADRRLRVMVQTECOVYVLAQCVR 301
DB	1902	VHCSAGVGRGTFTALDRILQDLSKDSVDIYGAVHADRRLRVMVQTECOVYVLAQCVR 1961
QY	302	DVLRARLRKLRSEHH 315

Db 1962 DVLARKLSEBOEN 1975

RESULT 2

US-09-949-016-8049
Sequence 8049, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8049
LENGTH: 1903
TYPE: PRT
ORGANISM: Human
US-09-949-016-8049

Query Match 94.3%; Score 1644; DB 2; Length 1903;
Best local similarity 97.5%; Pred. No. 7,4e-165;
Matches 306; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

QY 2 DRPLSHMLGQKGRKTSQPIKINQFEGHFMKLDNSNYLSKEYELKDVGRNOSCDI 61
DB 1574 DRPLSHMLGQK-----PIKINQFEGHFMKLDNSNYLSKEYELKDVGRNOSCDI 1627
QY 62 ALPBRGKRNILPYDAPATRYKLSNDDPCSDYINASYRGNNRREXYITQGPJRG 121
DB 1628 ALPBRGKRNILPYDAPATRYKLSNDDPCSDYINASYRGNNRREXYITQGPJRG 1687
QY 122 TKODFNKWEONVNIYVMTQCEKGRKCDHWYPADODSLYGDLLIQMLSESVLEW 181
DB 1688 TKODFNKWEONVNIYVMTQCEKGRKCDHWYPADODSLYGDLLIQMLSESVLEW 1747
QY 182 TIREFKICEBOLDARLIRHFIYVWPDHGVPTTOSLIQFRTVADYINRSPAGPTV 241
DB 1748 TIREFKICEBOLDARLIRHFIYVWPDHGVPTTOSLIQFRTVADYINRSPAGPTV 1807
QY 242 VHSAGVGTGTFIALDRILQQLSKDSVDIYGAVHDLRLHRVHWQTECOYVYLHQCVR 301
DB 1808 VHSAGVGTGTFIALDRILQQLSKDSVDIYGAVHDLRLHRVHWQTECOYVYLHQCVR 1867
QY 302 DVLARKLSEBOH 315
DB 1868 DVLARKLSEBOEN 1881

RESULT 3

US-08-201-697-16
Sequence 16, Application US/08201697
Patent No. 5705823
GENERAL INFORMATION:
APPLICANT: Miggins, Roger C.
APPLICANT: Thomas, Peedkayil E.
TITLE OF INVENTION: Mammalian Glomerular Epithelial Protein
NUMBER OF INVENTION: 1
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California

COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/201,697

FILING DATE: 25-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UM 9783

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 278 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-201-697-16

Query Match 82.8%; Score 1444; DB 1; Length 278;
Best local similarity 95.7%; Pred. No. 6,9e-145;
Matches 266; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 22 PIKINQFEGHFMKLDNSNYLSKEYELKDVGRNOSCDIALLPENRGRKRNINILPYDA 81
DB 1 PIKINQFEGHFMKLDNSNYLSKEYELKDVGRNOSCDIALLPENRGRKRNINILPYDA 60
QY 82 TRVLSNVDDPCSDYINASYRGNNRREXYITQGPJRGTDPMKQWVEONVNIYVW 141
DB 61 TRVLSNVDDPCSDYINASYRGNNRREXYITQGPJRGTDPMKQWVEONVNIYVW 120
QY 142 TOCEKGRKCDHWYPADODSLYGDLLIQMLSESVLEWPTIREFKICEBOLDARLIR 201
DB 121 TOCEKGRKCDHWYPADODSLYGDLLIQMLSESVLEWPTIREFKICEBOLDARLIR 180
QY 202 HHHTVWPDHGVPTTOSLIQFRTVADYINRSPAGPTVHSCAGVGTGTFIALDRIL 261
DB 181 HHHTVWPDHGVPTTOSLIQFRTVADYINRSPAGPTVHSCAGVGTGTFIALDRIL 240
QY 262 QQLDSKDSVDIYGAVHDLRLHRVHWQTECOYVYLHQC 299
DB 241 QQLDSKDSVDIYGAVHDLRLHRVHWQTECOYVYLHQC 278

RESULT 4

US-08-685-992-14
Sequence 14, Application US/08685992
Patent No. 5912138
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Millita Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/685,992
FILING DATE: 25-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-685-992-14

Query Match 78.8%; Score 1374; DB 1; Length 254;
Best Local Similarity 99.2%; Pred. No. 1,6e-137;
Matches 254; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 56 NOSCDIALPENGRKRNNTLPYDARVYLSNVDDPCSDYINASYIPGNPFREYIVT 115
DB 1 NOSCDIALPENGRKRNNTLPYDARVYLSNVDDPCSDYINASYIPGNPFREYIVT 60
QY 116 QGRLPTGDDPMKMEQVNIWVTVQCEKGRVKCDHWPADQSLYSGDLIQMLSE 175
DB 61 QGRLPTGDDPMKMEQVNIWVTVQCEKGRVKCDHWPADQSLYSGDLIQMLSE 120
QY 176 SVLEPMTREFKICGEEQLDAHLIRHFHYTWPDHGVPETTSLOFRTVRYINRSP 235
DB 121 SVLEPMT--FKICGEEQLDAHLIRHFHYTWPDHGVPETTSLOFRTVRYINRSP 178
QY 236 GAGPTVWCSAGVGRGTFTIALDRILQQLDSKDSVDIYGAVHDLRLHRYHVMVQTECOYV 295
DB 179 GAGPTVWCSAGVGRGTFTIALDRILQQLDSKDSVDIYGAVHDLRLHRYHVMVQTECOYV 238
QY 296 LHQCVRDVLRARKLRS 311
DB 239 LHQCVRDVLRARKLRS 254

RESULT 5
US-09-144-925-14
Sequence 14, Application US/09144925
Patent No. 5951979
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSER: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: TWO MILITIA DRIVE
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02421-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Patsseq for Windows version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,992
FILING DATE: July 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-03Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-144-925-14

Query Match 78.8%; Score 1374; DB 1; Length 254;
Best Local Similarity 99.2%; Pred. No. 1,6e-137;
Matches 254; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 56 NOSCDIALPENGRKRNNTLPYDARVYLSNVDDPCSDYINASYIPGNPFREYIVT 115
DB 1 NOSCDIALPENGRKRNNTLPYDARVYLSNVDDPCSDYINASYIPGNPFREYIVT 60
QY 116 QGRLPTGDDPMKMEQVNIWVTVQCEKGRVKCDHWPADQSLYSGDLIQMLSE 175
DB 61 QGRLPTGDDPMKMEQVNIWVTVQCEKGRVKCDHWPADQSLYSGDLIQMLSE 120
QY 176 SVLEPMTREFKICGEEQLDAHLIRHFHYTWPDHGVPETTSLOFRTVRYINRSP 235
DB 121 SVLEPMT--FKICGEEQLDAHLIRHFHYTWPDHGVPETTSLOFRTVRYINRSP 178
QY 236 GAGPTVWCSAGVGRGTFTIALDRILQQLDSKDSVDIYGAVHDLRLHRYHVMVQTECOYV 295
DB 179 GAGPTVWCSAGVGRGTFTIALDRILQQLDSKDSVDIYGAVHDLRLHRYHVMVQTECOYV 238
QY 296 LHQCVRDVLRARKLRS 311
DB 239 LHQCVRDVLRARKLRS 254

RESULT 6
US-08-854-585-2
Sequence 2, Application US/08854585
Patent No. 6114140
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K. and Stefan, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, Suite 6300
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,585
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/237,940
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.
 REGISTRATION NUMBER: 25,447
 REFERENCE/DOCKET NUMBER: 27866/31954
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1337 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-854-585-2

Query Match 50.4%; Score 878.5; DB 2; Length 1337;
 Best Local Similarity 56.4%; Pred. No. 98-84;
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;
 QY 18 KTSCPIKINOFEGHFMKLDADSNLSSKEYEELKDVGRNOSCDIALLEPENGKRRYNTL 77
 DB 1016 KSKSLIRVENFEAYFKQADSNCGFAEYEDLKVGISOPKXAELEENKRRYNTL 1075
 QY 78 PDATRYVLSNVDDPCSDYINASYIPGNFRREYIVTQGPLPGTKDDFWRMWMEQNVN 137
 DB 1076 PDISRVLKLS-VQTHSTDDYINAWMPGYHKKDFIATQGPLPLTKDPMRMWMEQNVYA 1134
 QY 138 IVMWTCVKGKRYKCDHWPADPSLYGDLILQMLSESVLPMTIRREFKICEBOLDAN 197
 DB 1135 IIMLKVEGGRKCEBYWPSKQ-ADYGDIVAMTSEIVLPMTIRDFVKNIQTSSEH 1193
 QY 198 RLIRHFRTWPHGVPETTSLOFRTVTRDYINRSPGAPTVVHCSAGVGRGTFFIL 257
 DB 1194 PL-RQFHTSPHGVPTDLDLINFRIYLRDMKQSPSPSPILVHCAGVGRGTFFIL 1252
 QY 258 DRIIQGLSDSYDIYGAVHDLRLRHVHNVQTECOYVYLHQCVRDYLAAR 308
 DB 1253 DRLIYQLENNIVDYGIYDLRHRPLMVQTEQDYVFLNQCVDIVASOK 1303

RESULT 7
 US-09-447-533-2
 Sequence 2, Application US/09447533
 Patent No. 6552169
 GENERAL INFORMATION:
 APPLICANT: Tonks, Nicholas K.
 Oelman, Arne
 TITLE OF INVENTION: DENSITY ENHANCED PROTEIN TYROSINE
 PHOSPHATASES
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed IP Law Group PLLC
 STREET: Suite 6300, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/447,533
 FILING DATE: 23-NOV-95
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Rosenman Ph.D., Stephen J.
 REGISTRATION NUMBER: 43,058
 REFERENCE/DOCKET NUMBER: 200125, 402C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1337 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-447-533-2

Query Match 50.4%; Score 878.5; DB 2; Length 1337;
 Best Local Similarity 56.4%; Pred. No. 98-84;
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;
 QY 18 KTSCPIKINOFEGHFMKLDADSNLSSKEYEELKDVGRNOSCDIALLEPENGKRRYNTL 77
 DB 1016 KSKSLIRVENFEAYFKQADSNCGFAEYEDLKVGISOPKXAELEENKRRYNTL 1075
 QY 78 PDATRYVLSNVDDPCSDYINASYIPGNFRREYIVTQGPLPGTKDDFWRMWMEQNVN 137
 DB 1076 PDISRVLKLS-VQTHSTDDYINAWMPGYHKKDFIATQGPLPLTKDPMRMWMEQNVYA 1134
 QY 138 IVMWTCVKGKRYKCDHWPADPSLYGDLILQMLSESVLPMTIRREFKICEBOLDAN 197
 DB 1135 IIMLKVEGGRKCEBYWPSKQ-ADYGDIVAMTSEIVLPMTIRDFVKNIQTSSEH 1193
 QY 198 RLIRHFRTWPHGVPETTSLOFRTVTRDYINRSPGAPTVVHCSAGVGRGTFFIL 257
 DB 1194 PL-RQFHTSPHGVPTDLDLINFRIYLRDMKQSPSPSPILVHCAGVGRGTFFIL 1252
 QY 258 DRIIQGLSDSYDIYGAVHDLRLRHVHNVQTECOYVYLHQCVRDYLAAR 308
 DB 1253 DRLIYQLENNIVDYGIYDLRHRPLMVQTEQDYVFLNQCVDIVASOK 1303

RESULT 8
 PCT-US95-05512-2
 Sequence 2, Application PC/TUS9505512
 GENERAL INFORMATION:
 APPLICANT: Tonks, Nicholas K. and stman, Arne
 TITLE OF INVENTION: Density Enhanced Protein Tyrosine
 PHOSPHATASE
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 STREET: 233 South Wacker Drive, Suite 6300
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/05512
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Borun, Michael F.
 REGISTRATION NUMBER: 25,447
 REFERENCE/DOCKET NUMBER: 27866/31954
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1337 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-05512-2
 Query Match 50.4%; Score 878.5; DB 4; Length 1337;

Best Local Similarity 56.4%; Pred. No. 9e-84;
Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;

QY 18 KTSCKPKNQEGHFMKLDNSNYLSKYEELKDVGRNOSCDIALPERKGRNNIL 77
DB 1016 KSKRLIRNENFAFKQKQDSCNCFEAEYEDLKGISQPRYALAEKRGKNNIVL 1075
QY 78 PYDATVYKLSNVDDPCSDYINASYIPGNRRREYIVTQGLPQTKDPMKRWMEQNNH 137
DB 1076 PYDISVYKLS-VQTHSTDDYINANNYPMYSHKQDFATQGLPPTLADPMRWMEQNNY 1134
QY 138 IYAVTQCEYKGRVAKDHYWPAODSLVYGDLLQMLSESVLPEWTIREPKICEBOLDH 197
DB 1135 IYVLTQCEYKGRVAKDHYWPAODSLVYGDLLQMLSESVLPEWTIREPKICEBOLDH 1193
QY 198 RLIRHRYTWPDHGVPEPTQSLIQFRTVYDYNRSFGAGPTVWCSAGVGRGTPTIAL 257
DB 1194 PL-RQHFTSPDHGVPEPTQSLIQFRTVYDYNRSFGAGPTVWCSAGVGRGTPTIAL 1252
QY 258 DRILQDSDSDYIYGAVHDLRLHRVWQTCQVYVHQCQVADVLARK 308
DB 1253 DRILQDSDSDYIYGAVHDLRLHRVWQTCQVYVHQCQVADVLARK 1303

RESULT 9
US-08-201-697-17
Sequence 17, Application US/08201697
Patent No. 5705623
GENERAL INFORMATION:
APPLICANT: Wiggins, Roger C.
TITLE OF INVENTION: Mammalian Glomerular Epithelial Protein
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/201,697
FILING DATE: 25-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UM 9783
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-201-697-17

Query Match 48.4%; Score 843.5; DB 1; Length 273;
Best Local Similarity 56.3%; Pred. No. 4.2e-81;
Matches 157; Conservative 44; Mismatches 71; Indels 7; Gaps 3;

QY 22 PIKINQEGHFMKLDNSNYLSKYEELKDVGRNOSCDIALPERKGRNNILPYDA 81
DB 1 PIKINQEGHFMKLDNSNYLSKYEELKDVGRNOSCDIALPERKGRNNILPYDA 60

QY 82 TRVLKSNVDDPCSDYINASYIPGNRRREYIVTQGLPQTKDPMKRWMEQNNIVM 141

DB 61 SHFLQVDDSDGSDYINANNYPMYSHKQDFATQGLPPTLADPMRWMEQNNY 120
QY 142 TQCEYKGRVAKDHYWPAODSLVYGDLLQMLSESVLPEWTIREPKICEBOLDH 200
DB 121 TQCEYKGRVAKDHYWPAODSLVYGDLLQMLSESVLPEWTIREPKICEBOLDH 176
QY 201 RHFTTWPDHGVPEPTQSLIQFRTVYDYNRSFGAGPTVWCSAGVGRGTPTIAL 260
DB 177 RHFTTWPDHGVPEPTQSLIQFRTVYDYNRSFGAGPTVWCSAGVGRGTPTIAL 234
QY 261 LQDSDSDYIYGAVHDLRLHRVWQTCQVYVHQCQVADVLARK 299
DB 235 LQDSDSDYIYGAVHDLRLHRVWQTCQVYVHQCQVADVLARK 273

RESULT 10
US-09-949-016-8833
Sequence 8833, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-07
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8833
LENGTH: 506
TYPE: PRT
ORGANISM: Human
US-09-949-016-8833

Query Match 43.9%; Score 765; DB 2; Length 506;
Best Local Similarity 48.2%; Pred. No. 2.3e-72;
Matches 147; Conservative 59; Mismatches 89; Indels 10; Gaps 4;

QY 2 DRPLSYVNLGQK--NRKTSCKPKNQEGHFMKLDNSNYLSKYEELKDVGRNOS 58
DB 184 DYLAFTYINPMKNGKLRKLTWVQDDFDAYIKMARDSDYKFSQFEELKLTGLDTP 243
QY 59 CDIALPERKGRNNILPYDATVYKLSNVDDPCSDYINASYIPGNRRREYIVTQGP 118
DB 244 HPAADPLERKGRNNILPYDPSKRVLSNREEGADYINANNYPMYSHKQDFATQGP 303
QY 119 LPTQDPMKRWMEQNNIVMOTQCEYKGRVAKDHYWPAODSLVYGDLLQMLSESVL 176
DB 304 LPTQDPMKRWMEQNNIVMOTQCEYKGRVAKDHYWPAODSLVYGDLLQMLSESVL 363
QY 179 PEWTIREPKICEBOLDHRLRHPRYTWPDHGVP--ETQSLIQFRTVYDYNRSFG 236
DB 364 DDMACRHFRI--NYADEMODVWHFRYTAMPDHGVPATANASIIQFVHVRQATKS-- 418
QY 237 AGPTVWCSAGVGRGTPTIALDRILQDSDSDYIYGAVHDLRLHRVWQTCQVYL 296
DB 419 KGPWTHCSAGVGRGTPTIALDRILQDSDSDYIYGAVHDLRLHRVWQTCQVYL 273

RESULT 11
US-09-949-016-8834
Sequence 8834, Application US/09949016

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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8834
LENGTH: 506
TYPE: PRT
ORGANISM: Human
US-09-949-016-8834

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```

Query Match 43.9%; Score 765; DB 2; Length 506;
Best Local Similarity 48.2%; Pred. No. 2.3e-72;
Matches 147; Conservative 59; Mismatches 89; Indels 10; Gaps 4;

```

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QY 2 DRPLSVHLNGGKG--NRKTSCKIKINQFEGHFMKLDASNYLSKEYEELKQVGRNOS 58
DB 184 DYLLAFYINPWSKNGKLGKRLTNVQLODFAYIKDWAQSDYKFSLOFEBELKIGLDIP 243
QY 59 CDIALPENRGKRNKRNITLIPYDATRYKLSNVDDPCSDYINASYIPGNFRREYIYTOGP 118
DB 244 HPAADLPANCKRRTNITLIPYDSRRLVSNBEGADYINANYIPGNSPOEYIATQGP 303
QY 119 LPTGTDPMKRWMEONVNIYMTQCEKRGKCDHWYPADDSLYYGDLLQWLSSEVL 178
DB 304 LPTGTDPMKRWMEONVNIYMTQCEKRGKCDHWYPADDSLYYGDLLQWLSSEVL 363
QY 179 PWTIRPEKICEBOLDHRLIRHPTVWPDGVP--ETTSLOIPRTVYDYNRSPG 236
DB 364 DMACHRFRI--NYADEMODVHFNTYAMPDGVPTANAAESILQFVHWROQATKS-- 418
QY 237 AGPTVHCSAGVGTGTFIALDRILQQLDSKDSVDYIGAVHDLRLHRYHNVOTECQYVL 296
DB 419 KGPMTIHCSAGVGTGTFIALDRILQHLIRHDFVILGLVSEMSYRMSVOTEBQYIFI 478
QY 297 HOCVR 301
DB 479 HOCVQ 483

```

```

RESULT 12
US-09-949-016-8835
Sequence 8835, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8835
LENGTH: 506
TYPE: PRT

```

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ORGANISM: Human
US-09-949-016-8835

```

```

Query Match 43.9%; Score 765; DB 2; Length 506;
Best Local Similarity 48.2%; Pred. No. 2.3e-72;
Matches 147; Conservative 59; Mismatches 89; Indels 10; Gaps 4;

```

```

QY 2 DRPLSVHLNGGKG--NRKTSCKIKINQFEGHFMKLDASNYLSKEYEELKQVGRNOS 58
DB 184 DYLLAFYINPWSKNGKLGKRLTNVQLODFAYIKDWAQSDYKFSLOFEBELKIGLDIP 243
QY 59 CDIALPENRGKRNKRNITLIPYDATRYKLSNVDDPCSDYINASYIPGNFRREYIYTOGP 118
DB 244 HPAADLPANCKRRTNITLIPYDSRRLVSNBEGADYINANYIPGNSPOEYIATQGP 303
QY 119 LPTGTDPMKRWMEONVNIYMTQCEKRGKCDHWYPADDSLYYGDLLQWLSSEVL 178
DB 304 LPTGTDPMKRWMEONVNIYMTQCEKRGKCDHWYPADDSLYYGDLLQWLSSEVL 363
QY 179 PWTIRPEKICEBOLDHRLIRHPTVWPDGVP--ETTSLOIPRTVYDYNRSPG 236
DB 364 DMACHRFRI--NYADEMODVHFNTYAMPDGVPTANAAESILQFVHWROQATKS-- 418
QY 237 AGPTVHCSAGVGTGTFIALDRILQQLDSKDSVDYIGAVHDLRLHRYHNVOTECQYVL 296
DB 419 KGPMTIHCSAGVGTGTFIALDRILQHLIRHDFVILGLVSEMSYRMSVOTEBQYIFI 478
QY 297 HOCVR 301
DB 479 HOCVQ 483

```

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RESULT 13
US-09-949-016-8836
Sequence 8836, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8836
LENGTH: 506
TYPE: PRT
ORGANISM: Human
US-09-949-016-8836

```

```

Query Match 43.9%; Score 765; DB 2; Length 506;
Best Local Similarity 48.2%; Pred. No. 2.3e-72;
Matches 147; Conservative 59; Mismatches 89; Indels 10; Gaps 4;

```

```

QY 2 DRPLSVHLNGGKG--NRKTSCKIKINQFEGHFMKLDASNYLSKEYEELKQVGRNOS 58
DB 184 DYLLAFYINPWSKNGKLGKRLTNVQLODFAYIKDWAQSDYKFSLOFEBELKIGLDIP 243
QY 59 CDIALPENRGKRNKRNITLIPYDATRYKLSNVDDPCSDYINASYIPGNFRREYIYTOGP 118
DB 244 HPAADLPANCKRRTNITLIPYDSRRLVSNBEGADYINANYIPGNSPOEYIATQGP 303
QY 119 LPTGTDPMKRWMEONVNIYMTQCEKRGKCDHWYPADDSLYYGDLLQWLSSEVL 178
DB 304 LPTGTDPMKRWMEONVNIYMTQCEKRGKCDHWYPADDSLYYGDLLQWLSSEVL 363

```

```

QY 179 PWTIRFKICGEBQDARLIRHFTYWPDPHVP--ETTSQILOFRTVADYINRSPG 236
DB 364 DWMACHRFRI---NYADEMOWMHNFTAMPDGVPTANNAESILQFVHVRQOATKS-- 418
QY 237 AGPTVHCSAGVGTGTFTFIALDRILQLODSKDSVDIYGAVHDLRLHRYVMVQTECOYVL 296
DB 419 KGPMTIHCSAGVGTGTFTFIALDRILQHIRDHEFVDILGLVSEMSYRSMNVQTECOYIFI 478
QY 297 HOCVR 301
DB 479 HOCVQ 483

```

RESULT 14
US-09-949-016-8837

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; Sequence 8837, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8837
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8837

```

Query Match 43.9%; Score 765; DB 2; Length 506;
Best Local Similarity 48.2%; Pred. No. 2,3e-72;
Matches 147; Conservative 59; Mismatches 89; Indels 10; Gaps 4;

```

QY 2 DRPLSVHNLGQXG---NKRKTSPIKINOPEGHFMKLOADSNYLLSKEYEELKDVGRNOS 58
DB 184 DYLLAFYINPMWSKXGKXKRLNVPQLDPDVAYIKDMAKSDYKFSLOPEELKJLGIDIP 243
QY 59 CDIALPEBKGNKRYNNILPYDATRYVLSVDDPCSDYINASYIPGNFRREYIVTQGP 118
DB 244 HPAAIDPLNRCRKNITNIPYDFSRVLSMNEBEGADYINANYIGVNSPQEIYATQGP 303
QY 119 LFGTDDPRKVMQVNVHNTVWTCVCEKRYKCHYTPADQDSLYYGLLIQMLSSVYL 178
DB 304 LPETRNDFPMKXVLDQKSOIIVMLTQCNCKRKYKCDHWPFTSEPIAYGDIIVEMISEEQ 363
QY 179 PWTIRFKICGEBQDARLIRHFTYWPDPHVP--ETTSQILOFRTVADYINRSPG 236
DB 364 DWMACHRFRI---NYADEMOWMHNFTAMPDGVPTANNAESILQFVHVRQOATKS-- 418
QY 237 AGPTVHCSAGVGTGTFTFIALDRILQLODSKDSVDIYGAVHDLRLHRYVMVQTECOYVL 296
DB 419 KGPMTIHCSAGVGTGTFTFIALDRILQHIRDHEFVDILGLVSEMSYRSMNVQTECOYIFI 478
QY 297 HOCVR 301
DB 479 HOCVQ 483

```

RESULT 15
US-09-949-016-8838
; Sequence 8838, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

```

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8838
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8838

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Query Match 43.9%; Score 765; DB 2; Length 506;
Best Local Similarity 48.2%; Pred. No. 2,3e-72;
Matches 147; Conservative 59; Mismatches 89; Indels 10; Gaps 4;

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QY 2 DRPLSVHNLGQXG---NKRKTSPIKINOPEGHFMKLOADSNYLLSKEYEELKDVGRNOS 58
DB 184 DYLLAFYINPMWSKXGKXKRLNVPQLDPDVAYIKDMAKSDYKFSLOPEELKJLGIDIP 243
QY 59 CDIALPEBKGNKRYNNILPYDATRYVLSVDDPCSDYINASYIPGNFRREYIVTQGP 118
DB 244 HPAAIDPLNRCRKNITNIPYDFSRVLSMNEBEGADYINANYIGVNSPQEIYATQGP 303
QY 119 LFGTDDPRKVMQVNVHNTVWTCVCEKRYKCHYTPADQDSLYYGLLIQMLSSVYL 178
DB 304 LPETRNDFPMKXVLDQKSOIIVMLTQCNCKRKYKCDHWPFTSEPIAYGDIIVEMISEEQ 363
QY 179 PWTIRFKICGEBQDARLIRHFTYWPDPHVP--ETTSQILOFRTVADYINRSPG 236
DB 364 DWMACHRFRI---NYADEMOWMHNFTAMPDGVPTANNAESILQFVHVRQOATKS-- 418
QY 237 AGPTVHCSAGVGTGTFTFIALDRILQLODSKDSVDIYGAVHDLRLHRYVMVQTECOYVL 296
DB 419 KGPMTIHCSAGVGTGTFTFIALDRILQHIRDHEFVDILGLVSEMSYRSMNVQTECOYIFI 478
QY 297 HOCVR 301
DB 479 HOCVQ 483

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Search completed: February 17, 2006, 01:26:31
Job time : 48 secs

GenCore version 5.1.7
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OW protein - protein search, using sw model

Run on: February 17, 2006, 01:36:29 / Search time 165 Seconds

(Without alignments)
807,803 Million cell updates/sec

Title: US-10-634-027-7

Perfect score: 1744

Sequence: 1 GDRPLSVHLNLGQKRNKRTS.....VEDYLARKLRSPQHNNHH 319

Scoring table: BLOSUM62

Gapop 10.0 / Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications_AA_Main:

1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1744	100.0	319	4	US-10-634-027-7
2	1691	97.0	319	4	US-10-634-027-7
3	1691	97.0	319	4	US-10-634-027-7
4	1691	97.0	319	4	US-10-634-027-7
5	1691	97.0	319	4	US-10-634-027-7
6	1691	97.0	319	4	US-10-634-027-7
7	1691	97.0	319	4	US-10-634-027-7
8	1691	97.0	319	4	US-10-634-027-7
9	1691	97.0	319	4	US-10-634-027-7
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18	1691	97.0	319	4	US-10-634-027-7
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23	1691	97.0	319	4	US-10-634-027-7
24	1691	97.0	319	4	US-10-634-027-7
25	1691	97.0	319	4	US-10-634-027-7
26	1691	97.0	319	4	US-10-634-027-7
27	1691	97.0	319	4	US-10-634-027-7

28	761.5	43.7	1188	5	US-10-029-345A-27	Sequence 27, Appl
29	744.5	42.7	309	3	US-09-788-626-16	Sequence 16, Appl
30	709.5	40.7	1093	4	US-10-245-539-4	Sequence 4, Appl
31	709.5	40.7	1118	4	US-10-245-539-2	Sequence 2, Appl
32	709.5	40.7	1118	4	US-10-245-539-8	Sequence 8, Appl
33	701	40.2	1167	4	US-10-369-493-5508	Sequence 5508, Ap
34	701	40.2	1167	4	US-10-369-493-5509	Sequence 5509, Ap
35	697.5	40.0	1111	5	US-10-029-345A-38	Sequence 38, Appl
36	697.5	38.7	2301	3	US-09-822-871-4	Sequence 4, Appl
37	675	38.7	2301	3	US-10-087-684-37	Sequence 37, Appl
38	675	38.7	2302	4	US-10-087-684-37	Sequence 37, Appl
39	675	38.7	2302	4	US-10-029-345A-37	Sequence 37, Appl
40	673.5	38.6	1705	5	US-10-314-232-15	Sequence 15, Appl
41	673	38.6	401	4	US-10-314-232-15	Sequence 22, Appl
42	673	38.6	898	4	US-10-466-759-2	Sequence 2, Appl
43	673	38.6	2299	4	US-10-087-684-10	Sequence 10, Appl
44	673	38.6	2300	4	US-10-218-779-10	Sequence 10, Appl
45	673	38.6	2300	4	US-10-218-779-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-634-027-7
Sequence 7, Application US/10634027
Publication No: US20040077065A1
GENERAL INFORMATION:
APPLICANT: Bioceleration, Artem G
APPLICANT: Bioceleration, Artem G
TITLE OF INVENTION: Three Dimensional Coordinates of HPTbeta
FILE REFERENCE: 9045M2
CURRENT FILING DATE: 2003-08-04
PRIORITY FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.2
SEQ ID NO 7
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens
US-10-634-027-7

Query Match	100.0%	Score 1744	DB 4	Length 319
Best Local Similarity	100.0%	Pred. No. 2.3e-158		
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D	1	GDRPLSVHLNLGQKRNKRTSCPIKINQFEGHFMKLDADSNYLSKEYEELKQVGRNOSCD	60	
Q	61	IALLPFRKRNKRNNTLPYATRYKLSNDDPCSDYINASTYRGNFRREYVTOGSLP	120	
D	61	IALLPFRKRNKRNNTLPYATRYKLSNDDPCSDYINASTYRGNFRREYVTOGSLP	120	
Q	121	GTQDPRKRNKRNNTLPYATRYKLSNDDPCSDYINASTYRGNFRREYVTOGSLP	180	
D	121	GTQDPRKRNKRNNTLPYATRYKLSNDDPCSDYINASTYRGNFRREYVTOGSLP	180	
Q	181	WTIRFKIGCEHOLDARLIRHRYTWPDHGVPETTSLOIPRYTRDYINRSFAGPT	240	
D	181	WTIRFKIGCEHOLDARLIRHRYTWPDHGVPETTSLOIPRYTRDYINRSFAGPT	240	
Q	241	VVHCSAGVGRSTFIALDRILQOLDSKOSVDIGAVHDLRLRHVAVQTECOVYLHOCV	300	
D	241	VVHCSAGVGRSTFIALDRILQOLDSKOSVDIGAVHDLRLRHVAVQTECOVYLHOCV	300	
Q	301	RDVLRARKLRSPQHNNHH 319		
D	301	RDVLRARKLRSPQHNNHH 319		


```

RESULT 2
US-10-634-027-4
Sequence 4, Application US/10634027
Publication No. US20040077065A1
GENERAL INFORMATION:
APPLICANT: Procter & Gamble Company
APPLICANT: Evdokimov, Artem G
APPLICANT: Pokros, Matthew E
TITLE OF INVENTION: Three Dimensional Coordinates of HPTbeta
FILE REFERENCE: 9045W2
CURRENT FILING DATE: 2003-08-04
PRIORITY FILING DATE: 2002-09-25
PRIORITY FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 336
TYPE: PRT
ORGANISM: Homo sapiens
US-10-634-027-4

Query Match
Best Local Similarity 97.0%; Score 1691; DB 4; Length 336;
Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DRPLSVHLNIGKGRKRTSCPIKINQFEGHFMKLDADSNVLLSKEYEELKDVGRNOSCDI 61
DB 1 DRPLSVHLNIGKGRKRTSCPIKINQFEGHFMKLDADSNVLLSKEYEELKDVGRNOSCDI 60
QY 62 ALPBNNGKRRNNILPYDATRVKLSNVDDPCSDYINASYIPGNFRREYIYTOGPIPG 121
DB 61 ALPBNNGKRRNNILPYDATRVKLSNVDDPCSDYINASYIPGNFRREYIYTOGPIPG 120
QY 122 TKDDPMWMEQWNVNIWYTCQVEKGRVCDHYWPAODDSLYGDDLILOMSESVLPBW 181
DB 121 TKDDPMWMEQWNVNIWYTCQVEKGRVCDHYWPAODDSLYGDDLILOMSESVLPBW 180
QY 182 TIREFKICEBOLDARLIRHRYTWPDHGVPTTOSLIQVRYVADYINRSPGAGPTV 241
DB 181 TIREFKICEBOLDARLIRHRYTWPDHGVPTTOSLIQVRYVADYINRSPGAGPTV 240
QY 242 VHCAGVGRGTGFIALDRILLOQDSDSDYDYGAVHDLRLHRYVWOTECQVYVYHOCVR 301
DB 241 VHCAGVGRGTGFIALDRILLOQDSDSDYDYGAVHDLRLHRYVWOTECQVYVYHOCVR 300
QY 302 DVLARKLRSEOH 315
DB 301 DVLARKLRSEOH 314

RESULT 3
US-09-909-567B-54
Sequence 54, Application US/09909567B
Publication No. US20030022257A1
GENERAL INFORMATION:
APPLICANT: Macina, Roberto A.
APPLICANT: Nait, Mamou
APPLICANT: Chan, Selva
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
FILE REFERENCE: DEX-0214
CURRENT FILING DATE: 2001-07-20
PRIORITY FILING DATE: 2000-07-21
PRIORITY FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn version 3.1
SEQ ID NO 54
LENGTH: 1997
TYPE: PRT
ORGANISM: Homo sapiens
US-09-909-567B-54

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Query Match
Best Local Similarity 97.0%; Score 1691; DB 3; Length 1997;
Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DRPLSVHLNIGKGRKRTSCPIKINQFEGHFMKLDADSNVLLSKEYEELKDVGRNOSCDI 61
DB 1662 DRPLSVHLNIGKGRKRTSCPIKINQFEGHFMKLDADSNVLLSKEYEELKDVGRNOSCDI 1721
QY 62 ALPBNNGKRRNNILPYDATRVKLSNVDDPCSDYINASYIPGNFRREYIYTOGPIPG 121
DB 61 ALPBNNGKRRNNILPYDATRVKLSNVDDPCSDYINASYIPGNFRREYIYTOGPIPG 120
QY 122 TKDDPMWMEQWNVNIWYTCQVEKGRVCDHYWPAODDSLYGDDLILOMSESVLPBW 181
DB 121 TKDDPMWMEQWNVNIWYTCQVEKGRVCDHYWPAODDSLYGDDLILOMSESVLPBW 180
QY 182 TIREFKICEBOLDARLIRHRYTWPDHGVPTTOSLIQVRYVADYINRSPGAGPTV 241
DB 181 TIREFKICEBOLDARLIRHRYTWPDHGVPTTOSLIQVRYVADYINRSPGAGPTV 240
QY 242 VHCAGVGRGTGFIALDRILLOQDSDSDYDYGAVHDLRLHRYVWOTECQVYVYHOCVR 301
DB 241 VHCAGVGRGTGFIALDRILLOQDSDSDYDYGAVHDLRLHRYVWOTECQVYVYHOCVR 300
QY 302 DVLARKLRSEOH 315
DB 1902 VHCAGVGRGTGFIALDRILLOQDSDSDYDYGAVHDLRLHRYVWOTECQVYVYHOCVR 1961
QY 1902 VHCAGVGRGTGFIALDRILLOQDSDSDYDYGAVHDLRLHRYVWOTECQVYVYHOCVR 1961
DB 1962 DVLARKLRSEOH 1975

RESULT 4
US-10-634-027-2
Sequence 2, Application US/10634027
Publication No. US20040077065A1
GENERAL INFORMATION:
APPLICANT: Procter & Gamble Company
APPLICANT: Evdokimov, Artem G
APPLICANT: Pokros, Matthew E
TITLE OF INVENTION: Three Dimensional Coordinates of HPTbeta
FILE REFERENCE: 9045W2
CURRENT FILING DATE: 2003-08-04
PRIORITY FILING DATE: 2002-09-25
PRIORITY FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 1997
TYPE: PRT
ORGANISM: Homo sapiens
US-10-634-027-2

Query Match
Best Local Similarity 97.0%; Score 1691; DB 4; Length 1997;
Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DRPLSVHLNIGKGRKRTSCPIKINQFEGHFMKLDADSNVLLSKEYEELKDVGRNOSCDI 61
DB 1662 DRPLSVHLNIGKGRKRTSCPIKINQFEGHFMKLDADSNVLLSKEYEELKDVGRNOSCDI 1721
QY 62 ALPBNNGKRRNNILPYDATRVKLSNVDDPCSDYINASYIPGNFRREYIYTOGPIPG 121
DB 61 ALPBNNGKRRNNILPYDATRVKLSNVDDPCSDYINASYIPGNFRREYIYTOGPIPG 120
QY 122 TKDDPMWMEQWNVNIWYTCQVEKGRVCDHYWPAODDSLYGDDLILOMSESVLPBW 181
DB 121 TKDDPMWMEQWNVNIWYTCQVEKGRVCDHYWPAODDSLYGDDLILOMSESVLPBW 180
QY 182 TIREFKICEBOLDARLIRHRYTWPDHGVPTTOSLIQVRYVADYINRSPGAGPTV 241
DB 181 TIREFKICEBOLDARLIRHRYTWPDHGVPTTOSLIQVRYVADYINRSPGAGPTV 240
QY 242 VHCAGVGRGTGFIALDRILLOQDSDSDYDYGAVHDLRLHRYVWOTECQVYVYHOCVR 301
DB 241 VHCAGVGRGTGFIALDRILLOQDSDSDYDYGAVHDLRLHRYVWOTECQVYVYHOCVR 300
QY 302 DVLARKLRSEOH 315
DB 1902 VHCAGVGRGTGFIALDRILLOQDSDSDYDYGAVHDLRLHRYVWOTECQVYVYHOCVR 1961
QY 1902 VHCAGVGRGTGFIALDRILLOQDSDSDYDYGAVHDLRLHRYVWOTECQVYVYHOCVR 1961
DB 1962 DVLARKLRSEOH 1975

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Db      1902 VHSASVGRGTGFALDRILLOQDSKDSVDIYGAVHDLRLHRVAVQTECOYVYLHQCVR 1961
Qy      302 DVLRARKLRSEOH 315
Db      1962 DVLRARKLRSEOH 1975

RESULT 5
US-10-408-765A-2135
; Sequence 2135, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Bojin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; PRIORITY FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: Res-Seq for Windows Version 4.0
; SEQ ID NO 2135
; LENGTH: 1997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2135

Query Match      97.0%; Score 1691; DB 4; Length 1997;
Best Local Similarity 99.4%; Pred. No. 3.3e-152;
Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 DRPLSVHNLGQKGNRTSCPIKINQFEGHFMKLQADSNYLLSKYEYELKDVGRNOSCDI 61
Db      1662 DRPLSVHNLGQKGNRTSCPIKINQFEGHFMKLQADSNYLLSKYEYELKDVGRNOSCDI 1721
Qy      62 ALPENRGKRNYYNLLPYDATRVKLSNVDDPCSDYINASYIPGNFRREYIVTGGPLPG 121
Db      1722 ALPENRGKRNYYNLLPYDATRVKLSNVDDPCSDYINASYIPGNFRREYIVTGGPLPG 1781
Qy      122 TKDDFKMVMWGANVHNIWVWTCCKGKRVKCHYMPADODSLYYGDLILQMSSEVLPW 181
Db      1782 TKDDFKMVMWGANVHNIWVWTCCKGKRVKCHYMPADODSLYYGDLILQMSSEVLPW 1841
Qy      182 TIREFKICEGOLDARLIRHRYTWMPDHGVETTSGLIOFVATRVDTYINSRGAQPTV 241
Db      1842 TIREFKICEGOLDARLIRHRYTWMPDHGVETTSGLIOFVATRVDTYINSRGAQPTV 1901
Qy      242 VHSASVGRGTGFALDRILLOQDSKDSVDIYGAVHDLRLHRVAVQTECOYVYLHQCVR 301
Db      1902 VHSASVGRGTGFALDRILLOQDSKDSVDIYGAVHDLRLHRVAVQTECOYVYLHQCVR 1961
Qy      302 DVLRARKLRSEOH 315
Db      1962 DVLRARKLRSEOH 1975

RESULT 6
US-10-497-692-4
; Sequence 4, Application US/10497692
; Publication No. US20050004056A1
; GENERAL INFORMATION:
; APPLICANT: Meise, Martin
; APPLICANT: Eulenberg, Karsten
; APPLICANT: Fritsch, Rüdiger
; APPLICANT: Hader, Thomas
; APPLICANT: Bromer, Günter
; APPLICANT: Steuernagel, Arnd

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; TITLE OF INVENTION: Prp10d, Tec protein tyrosine kinase and EDRP homologous protei
; TITLE OF INVENTION: Involved in the regulation of energy homeostasis
; FILE REFERENCE: 2923-632
; CURRENT APPLICATION NUMBER: US/10/497,692
; PRIORITY FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: PCT/EP02/13744
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: EP 01 000 010.5
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: EP 01 129 138.2
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: EP 01 128 844.6
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-497-692-4

Query Match      97.0%; Score 1691; DB 5; Length 1997;
Best Local Similarity 99.4%; Pred. No. 3.3e-152;
Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 DRPLSVHNLGQKGNRTSCPIKINQFEGHFMKLQADSNYLLSKYEYELKDVGRNOSCDI 61
Db      1662 DRPLSVHNLGQKGNRTSCPIKINQFEGHFMKLQADSNYLLSKYEYELKDVGRNOSCDI 1721
Qy      62 ALPENRGKRNYYNLLPYDATRVKLSNVDDPCSDYINASYIPGNFRREYIVTGGPLPG 121
Db      1722 ALPENRGKRNYYNLLPYDATRVKLSNVDDPCSDYINASYIPGNFRREYIVTGGPLPG 1781
Qy      122 TKDDFKMVMWGANVHNIWVWTCCKGKRVKCHYMPADODSLYYGDLILQMSSEVLPW 181
Db      1782 TKDDFKMVMWGANVHNIWVWTCCKGKRVKCHYMPADODSLYYGDLILQMSSEVLPW 1841
Qy      182 TIREFKICEGOLDARLIRHRYTWMPDHGVETTSGLIOFVATRVDTYINSRGAQPTV 241
Db      1842 TIREFKICEGOLDARLIRHRYTWMPDHGVETTSGLIOFVATRVDTYINSRGAQPTV 1901
Qy      242 VHSASVGRGTGFALDRILLOQDSKDSVDIYGAVHDLRLHRVAVQTECOYVYLHQCVR 301
Db      1902 VHSASVGRGTGFALDRILLOQDSKDSVDIYGAVHDLRLHRVAVQTECOYVYLHQCVR 1961
Qy      302 DVLRARKLRSEOH 315
Db      1962 DVLRARKLRSEOH 1975

RESULT 7
US-10-756-149-5168
; Sequence 5168, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Zlotnik, Albea
; APPLICANT: Zlotnik, Albea
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER. COMPOSITIONS
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; PRIORITY FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5168
; LENGTH: 1997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-756-149-5168

Query Match      97.0%; Score 1691; DB 5; Length 1997;
Best Local Similarity 99.4%; Pred. No. 3.3e-152;
Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 2 DRPLSVHLNIGQKGRKTSQPIKINOFEGHFMKIQADSNVLSKEYEELKDVGKNSCDI 61
Db 1662 DRPLSVHLNIGQKGRKTSQPIKINOFEGHFMKIQADSNVLSKEYEELKDVGKNSCDI 1721
Qy 62 ALLEPENGKRRNNILPYDARVYKLSNVDDPCSDYINNSYIPGNPFREYITVQGPPLG 121
Db 1722 ALLEPENGKRRNNILPYDARVYKLSNVDDPCSDYINNSYIPGNPFREYITVQGPPLG 1781
Qy 122 TKDDFMQWMEQWENINIVMTQCEKGRKCDHYWPAADDSLYYGDLLQMLSESVLPFW 181
Db 1782 TKDDFMQWMEQWENINIVMTQCEKGRKCDHYWPAADDSLYYGDLLQMLSESVLPFW 1841
Qy 182 TIREFKICGEBOLDARHLIRHFHYTWDPHGVPETTSOLIOFRTVRDYINRSPGAGPTV 241
Db 1842 TIREFKICGEBOLDARHLIRHFHYTWDPHGVPETTSOLIOFRTVRDYINRSPGAGPTV 1901
Qy 242 VHCASAGVGRGTFIALDRILLOQLDSKDSVDIYGAVHDLRLHVRVWQTECOVYVYHQCVR 301
Db 1902 VHCASAGVGRGTFIALDRILLOQLDSKDSVDIYGAVHDLRLHVRVWQTECOVYVYHQCVR 1961
Qy 302 DVLARKLRSEQH 315
Db 1962 DVLARKLRSEQH 1975

RESULT 8
US-10-634-027-6
/ Sequence 6, Application US/10634027
/ Publication No. US20040077065M1
/ GENERAL INFORMATION:
/ APPLICANT: Procter & Gamble Company
/ APPLICANT: Evdokimov, Artem G
/ APPLICANT: Pokrosh, Matthew B
/ TITLE OF INVENTION: Three Dimensional Coordinates of HPTpbeta
/ FILE REFERENCE: 9045M2
/ CURRENT APPLICATION NUMBER: US/10/634,027
/ CURRENT FILING DATE: 2003-08-04
/ PRIOR APPLICATION NUMBER: US 60/413,547
/ PRIOR FILING DATE: 2002-09-25
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 6
/ LENGTH: 312
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-634-027-6

Query Match 96.9%; Score 1690; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 3.3e-153;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DRPLSVHLNIGQKGRKTSQPIKINOFEGHFMKIQADSNVLSKEYEELKDVGKNSCDI 61
Db 1 DRPLSVHLNIGQKGRKTSQPIKINOFEGHFMKIQADSNVLSKEYEELKDVGKNSCDI 60
Qy 62 ALLEPENGKRRNNILPYDARVYKLSNVDDPCSDYINNSYIPGNPFREYITVQGPPLG 121
Db 61 ALLEPENGKRRNNILPYDARVYKLSNVDDPCSDYINNSYIPGNPFREYITVQGPPLG 120
Qy 122 TKDDFMQWMEQWENINIVMTQCEKGRKCDHYWPAADDSLYYGDLLQMLSESVLPFW 181
Db 121 TKDDFMQWMEQWENINIVMTQCEKGRKCDHYWPAADDSLYYGDLLQMLSESVLPFW 180
Qy 182 TIREFKICGEBOLDARHLIRHFHYTWDPHGVPETTSOLIOFRTVRDYINRSPGAGPTV 241
Db 181 TIREFKICGEBOLDARHLIRHFHYTWDPHGVPETTSOLIOFRTVRDYINRSPGAGPTV 240
Qy 242 VHCASAGVGRGTFIALDRILLOQLDSKDSVDIYGAVHDLRLHVRVWQTECOVYVYHQCVR 301
Db 241 VHCASAGVGRGTFIALDRILLOQLDSKDSVDIYGAVHDLRLHVRVWQTECOVYVYHQCVR 300
Qy 302 DVLARKLRSEQ 313

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Db 301 DVLARKLRSEQ 312

RESULT 9
US-10-497-692-14
/ Sequence 14, Application US/10497692
/ Publication No. US2005004056M1
/ GENERAL INFORMATION:
/ APPLICANT: Meise, Martin
/ APPLICANT: Eulenberg, Karsten
/ APPLICANT: Fritsch, Rudiger
/ APPLICANT: Hader, Thomas
/ APPLICANT: Bronner, Gunter
/ APPLICANT: Steierhagel, Arnd
/ TITLE OF INVENTION: Ept10D, Tec protein tyrosine kinase and EPT1 homologous protein
/ FILE REFERENCE: 2923-632
/ CURRENT APPLICATION NUMBER: US/10/497,692
/ CURRENT FILING DATE: 2004-06-04
/ PRIOR APPLICATION NUMBER: PCT/EP02/13744
/ PRIOR FILING DATE: 2002-12-04
/ PRIOR APPLICATION NUMBER: EP 01 000 010.5
/ PRIOR FILING DATE: 2002-01-02
/ PRIOR APPLICATION NUMBER: EP 01 129 138.2
/ PRIOR FILING DATE: 2001-12-07
/ PRIOR APPLICATION NUMBER: EP 01 128 844.6
/ PRIOR FILING DATE: 2001-12-04
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 14
/ LENGTH: 1450
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-497-692-14

Query Match 95.6%; Score 1667; DB 5; Length 1450;
Best Local Similarity 100.0%; Pred. No. 4.2e-150;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DRPLSVHLNIGQKGRKTSQPIKINOFEGHFMKIQADSNVLSKEYEELKDVGKNSCDI 61
Db 1144 DRPLSVHLNIGQKGRKTSQPIKINOFEGHFMKIQADSNVLSKEYEELKDVGKNSCDI 1203
Qy 62 ALLEPENGKRRNNILPYDARVYKLSNVDDPCSDYINNSYIPGNPFREYITVQGPPLG 121
Db 1204 ALLEPENGKRRNNILPYDARVYKLSNVDDPCSDYINNSYIPGNPFREYITVQGPPLG 1263
Qy 122 TKDDFMQWMEQWENINIVMTQCEKGRKCDHYWPAADDSLYYGDLLQMLSESVLPFW 181
Db 1264 TKDDFMQWMEQWENINIVMTQCEKGRKCDHYWPAADDSLYYGDLLQMLSESVLPFW 1323
Qy 182 TIREFKICGEBOLDARHLIRHFHYTWDPHGVPETTSOLIOFRTVRDYINRSPGAGPTV 241
Db 1324 TIREFKICGEBOLDARHLIRHFHYTWDPHGVPETTSOLIOFRTVRDYINRSPGAGPTV 1383
Qy 242 VHCASAGVGRGTFIALDRILLOQLDSKDSVDIYGAVHDLRLHVRVWQTECOVYVYHQCVR 301
Db 1384 VHCASAGVGRGTFIALDRILLOQLDSKDSVDIYGAVHDLRLHVRVWQTECOVYVYHQCVR 1443
Qy 302 DVLARK 308
Db 1444 DVLARK 1450

RESULT 10
US-09-788-626-15
/ Sequence 15, Application US/09788626
/ Patent No. US20020009762M1
/ GENERAL INFORMATION:
/ APPLICANT: Cioot, Andrew J.
/ APPLICANT: Cool, Deborah E.
/ TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE

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TITLE OF INVENTION: PHOSPHATASES
 FILE REFERENCE: 200125.401
 CURRENT APPLICATION NUMBER: US/09/786.626
 CURRENT FILING DATE: 2001-02-13
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 15
 LENGTH: 310
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-786-626-15

Query Match 78.8%; Score 1374; DB 3; Length 310;
 Best Local Similarity 59.2%; Pred. No. 6,4e-123;
 Matches 254; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 56 NOSCIALLPENRGRKRNINILPYDAFRVLSVDDDCSDYINASYIPGNFRREYIVT 115
 DB 1 NOSCIALLPENRGRKRNINILPYDAFRVLSVDDDCSDYINASYIPGNFRREYIVT 60
 QY 116 OGPFGTDDPMKMWKQWQVNHVWVQVCEKGRYKCDHPADDSLYGDLILQMLSE 175
 DB 61 OGPFGTDDPMKMWKQWQVNHVWVQVCEKGRYKCDHPADDSLYGDLILQMLSE 120
 QY 176 SVLPETIREKICGSEQLDARLIRHPTTWPHGVPETTSILQFRVRYDYNRSP 235
 DB 121 SVLPETIREKICGSEQLDARLIRHPTTWPHGVPETTSILQFRVRYDYNRSP 178
 QY 236 GAGPTVWCSAGVGRGTFTIALDRILQDLSKOSVDIYGAVHDLRLHVMVQTECYIVT 295
 DB 179 GAGPTVWCSAGVGRGTFTIALDRILQDLSKOSVDIYGAVHDLRLHVMVQTECYIVT 238
 QY 296 LHQCVRDVLRARLRS 311
 DB 239 LHQCVRDVLRARLRS 254

RESULT 11
 US-10-723-606-3
 Sequence 3, Application US/10723606
 Publication No. US20040161821A1
 GENERAL INFORMATION:
 APPLICANT: Tonks, Nicholas K.
 TITLE OF INVENTION: DEP-1 RECEPTOR PROTEIN TYROSINE
 TITLE OF INVENTION: PHOSPHATASE INTERACTING PROTEINS
 TITLE OF INVENTION: AND RELATED METHODS
 FILE REFERENCE: 200125.447
 CURRENT APPLICATION NUMBER: US/10/723.606
 CURRENT FILING DATE: 2003-11-26
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 341
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-723-606-3

Query Match 50.4%; Score 878.5; DB 4; Length 341;
 Best Local Similarity 56.4%; Pred. No. 2.3e-75;
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;

QY 18 KTSCKIKNOFEGHFKLQADSNYLSKEYEELKDVGNOSCDIALLPENRGRKRNINIL 77
 DB 20 KTSCKIKNOFEGHFKLQADSNYLSKEYEELKDVGNOSCDIALLPENRGRKRNINIL 79
 QY 78 PYDATRVKLSNVDDPCSDYINASYIPGNFRREYIVTQGPLGTQDDPMKMWKQWQVNH 137
 DB 80 PYDATRVKLSNVDDPCSDYINASYIPGNFRREYIVTQGPLGTQDDPMKMWKQWQVNH 138
 QY 138 IYMTVQCEKGRYKCDHPADDSLYGDLILQMLSESVLPETIREKICGSEQLDAR 197
 DB 139 IYMTVQCEKGRYKCDHPADDSLYGDLILQMLSESVLPETIREKICGSEQLDAR 197

QY 198 RLIRHPTTWPHGVPETTSILQFRVRYDYNRSPGAGPTVWCSAGVGRGTFTIAL 257
 DB 198 RLIRHPTTWPHGVPETTSILQFRVRYDYNRSPGAGPTVWCSAGVGRGTFTIAL 256
 QY 258 DRILQDLSKOSVDIYGAVHDLRLHVMVQTECYIVTQGPLGTQDDPMKMWKQWQVNH 308
 DB 257 DRILQDLSKOSVDIYGAVHDLRLHVMVQTECYIVTQGPLGTQDDPMKMWKQWQVNH 307

RESULT 12
 US-10-390-501-2

Sequence 2, Application US/10390501
 Publication No. US20030148491A1
 GENERAL INFORMATION:
 APPLICANT: Tonks, Nicholas K.
 TITLE OF INVENTION: DENSITY ENHANCED PROTEIN TYROSINE
 PHOSPHATASES

NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESS: Seed IP Law Group PLLC
 STREET: Suite 6300, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/390.501
 FILING DATE: 13-Mar-2003
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Roseman Ph.D., Stephen J.
 REGISTRATION NUMBER: 43,058
 REFERENCE/DOCKET NUMBER: 200125.402C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1337 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-390-501-2

Query Match 50.4%; Score 878.5; DB 4; Length 1337;
 Best Local Similarity 56.4%; Pred. No. 1.4e-74;
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;

QY 18 KTSCKIKNOFEGHFKLQADSNYLSKEYEELKDVGNOSCDIALLPENRGRKRNINIL 77
 DB 1016 KTSCKIKNOFEGHFKLQADSNYLSKEYEELKDVGNOSCDIALLPENRGRKRNINIL 1075
 QY 78 PYDATRVKLSNVDDPCSDYINASYIPGNFRREYIVTQGPLGTQDDPMKMWKQWQVNH 137
 DB 1076 PYDATRVKLSNVDDPCSDYINASYIPGNFRREYIVTQGPLGTQDDPMKMWKQWQVNH 1134
 QY 138 IYMTVQCEKGRYKCDHPADDSLYGDLILQMLSESVLPETIREKICGSEQLDAR 197
 DB 1135 IYMTVQCEKGRYKCDHPADDSLYGDLILQMLSESVLPETIREKICGSEQLDAR 1193
 QY 198 RLIRHPTTWPHGVPETTSILQFRVRYDYNRSPGAGPTVWCSAGVGRGTFTIAL 257
 DB 1194 RLIRHPTTWPHGVPETTSILQFRVRYDYNRSPGAGPTVWCSAGVGRGTFTIAL 1252
 QY 258 DRILQDLSKOSVDIYGAVHDLRLHVMVQTECYIVTQGPLGTQDDPMKMWKQWQVNH 308

DB 1253 DRLIYQIENNTVDYGIYDLRMHRPLMVQTEDOYVFLNQCVDIVASOK 1303

RESULT 13

US-10-366-547-42
 ; Sequence 42, Application US/10366547
 ; Publication No. US20030215899A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meng, Tzu-Ching
 ; APPLICANT: Tonks, Nicholas K.
 ; APPLICANT: Cook, Deborah B.
 ; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
 ; FILE REFERENCE: 200125.439
 ; CURRENT APPLICATION NUMBER: US/10/366,547
 ; CURRENT FILING DATE: 2003-02-12
 ; NUMBER OF SEQ ID NOS: 98
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 42
 ; LENGTH: 1337
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-366-547-42

Query Match 50.4%; Score 878.5; DB 4; Length 1337;
 Best Local Similarity 56.4%; Pred. No. 1.4e-74;
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;

QY 18 KTSCPIKINQFEGHFMKLOADSNLTSKEYEELKDVGRNOSCDIALLENNRGNRRNNIL 77
 DB 1016 KSKSLIRVENFEAYFFKQOADSNGRAEYEDLKVGISQPKYALLENRGNRRNNIL 1075
 QY 78 PYDATRYVLSNVDDPCSDYINASYIPGNFRREYIVTQGLPGLTQDPFKRWMEQNVAN 137
 DB 1076 PYDISRVYLS-VQTHSTDDYINANYMPGYHSKQFIATQGPLNLTQDPFKRWMEQNVYA 1134
 QY 138 IVMATQCEKGRKCDHYMPADQDSLTYGDLILQMLSESYLPEWTIRREFKICGEQOLDAN 197
 DB 1133 IIMTKCEVGRKCEBYWPSKQ-AADYGDITVAMTSEIVLPEWTIRDFVKNIQTSSEH 1193
 QY 198 RLIRHFHYTWPDHGPVETQSILQFRTVRDYINRSPGAPTVVHCAGVGRGTGFIAL 257
 DB 1194 PL-RQFHTSMRPHGVPTDILINFRYLVNRDYMKSPPSPFLVHCAGVGRGTGFI 1252
 QY 258 DRLIQQDSDSDYDIYGAVHDLRLHRVHVQTECOYVYLHQCVRDVLARK 308
 DB 1253 DRLIYQIENNTVDYGIYDLRMHRPLMVQTEDOYVFLNQCVDIVASOK 1303

RESULT 14

US-10-366-547-44
 ; Sequence 44, Application US/10366547
 ; Publication No. US20030215899A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meng, Tzu-Ching
 ; APPLICANT: Tonks, Nicholas K.
 ; APPLICANT: Cook, Deborah B.
 ; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
 ; FILE REFERENCE: 200125.439
 ; CURRENT APPLICATION NUMBER: US/10/366,547
 ; CURRENT FILING DATE: 2003-02-12
 ; NUMBER OF SEQ ID NOS: 98
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 44
 ; LENGTH: 1337
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-366-547-44

Query Match 50.4%; Score 878.5; DB 4; Length 1337;
 Best Local Similarity 56.4%; Pred. No. 1.4e-74;

Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;
 QY 18 KTSCPIKINQFEGHFMKLOADSNLTSKEYEELKDVGRNOSCDIALLENNRGNRRNNIL 77
 DB 1016 KSKSLIRVENFEAYFFKQOADSNGRAEYEDLKVGISQPKYALLENRGNRRNNIL 1075
 QY 78 PYDATRYVLSNVDDPCSDYINASYIPGNFRREYIVTQGLPGLTQDPFKRWMEQNVAN 137
 DB 1076 PYDISRVYLS-VQTHSTDDYINANYMPGYHSKQFIATQGPLNLTQDPFKRWMEQNVYA 1134
 QY 138 IVMATQCEKGRKCDHYMPADQDSLTYGDLILQMLSESYLPEWTIRREFKICGEQOLDAN 197
 DB 1133 IIMTKCEVGRKCEBYWPSKQ-AADYGDITVAMTSEIVLPEWTIRDFVKNIQTSSEH 1193
 QY 198 RLIRHFHYTWPDHGPVETQSILQFRTVRDYINRSPGAPTVVHCAGVGRGTGFIAL 257
 DB 1194 PL-RQFHTSMRPHGVPTDILINFRYLVNRDYMKSPPSPFLVHCAGVGRGTGFI 1252
 QY 258 DRLIQQDSDSDYDIYGAVHDLRLHRVHVQTECOYVYLHQCVRDVLARK 308
 DB 1253 DRLIYQIENNTVDYGIYDLRMHRPLMVQTEDOYVFLNQCVDIVASOK 1303

RESULT 15

US-10-723-606-2
 ; Sequence 2, Application US/10723606
 ; Publication No. US20040161821A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Palke-Hamblin, Helena L.
 ; APPLICANT: Tonks, Nicholas K.
 ; TITLE OF INVENTION: DEP-1 RECEPTOR PROTEIN TYROSINE
 ; TITLE OF INVENTION: PHOSPHATASE INTERACTING PROTEINS
 ; FILE REFERENCE: 200125.447
 ; CURRENT APPLICATION NUMBER: US/10/723,606
 ; CURRENT FILING DATE: 2003-11-26
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 1337
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-723-606-2

Query Match 50.4%; Score 878.5; DB 4; Length 1337;
 Best Local Similarity 56.4%; Pred. No. 1.4e-74;
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;

QY 18 KTSCPIKINQFEGHFMKLOADSNLTSKEYEELKDVGRNOSCDIALLENNRGNRRNNIL 77
 DB 1016 KSKSLIRVENFEAYFFKQOADSNGRAEYEDLKVGISQPKYALLENRGNRRNNIL 1075
 QY 78 PYDATRYVLSNVDDPCSDYINASYIPGNFRREYIVTQGLPGLTQDPFKRWMEQNVAN 137
 DB 1076 PYDISRVYLS-VQTHSTDDYINANYMPGYHSKQFIATQGPLNLTQDPFKRWMEQNVYA 1134
 QY 138 IVMATQCEKGRKCDHYMPADQDSLTYGDLILQMLSESYLPEWTIRREFKICGEQOLDAN 197
 DB 1133 IIMTKCEVGRKCEBYWPSKQ-AADYGDITVAMTSEIVLPEWTIRDFVKNIQTSSEH 1193
 QY 198 RLIRHFHYTWPDHGPVETQSILQFRTVRDYINRSPGAPTVVHCAGVGRGTGFIAL 257
 DB 1194 PL-RQFHTSMRPHGVPTDILINFRYLVNRDYMKSPPSPFLVHCAGVGRGTGFI 1252
 QY 258 DRLIQQDSDSDYDIYGAVHDLRLHRVHVQTECOYVYLHQCVRDVLARK 308
 DB 1253 DRLIYQIENNTVDYGIYDLRMHRPLMVQTEDOYVFLNQCVDIVASOK 1303

Search completed: February 17, 2006, 01:39:43
 Job time : 166 secs

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OM protein - protein search, using sw model

Run on: February 17, 2006, 01:37:04, Search time 18 Seconds
(without alignments)
251,915 Million cell updates/sec

Title: US-10-634-027-7
Perfect score: 1744
Sequence: 1 GRPPLSVHLNIGQKGRKTS.....VEDVLRARAKLRSEQHRRHHH 319

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: Published Applications_A New:

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2: /cgn2_6/ptcdat1/pubpaa/US06_NEW_PUB pep: *
3: /cgn2_6/ptcdat1/pubpaa/US07_NEW_PUB pep: *
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8: /cgn2_6/ptcdat1/pubpaa/US13_NEW_PUB pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	878.5	50.4	1337	US-11-112-304A-33	Sequence 33, Appl
2	876.5	50.3	1178	US-10-995-861-851	Sequence 28, Appl
3	769	44.0	405	US-11-143-984A-28	Sequence 28, Appl
4	761.5	43.7	1188	US-11-143-984A-27	Sequence 38, Appl
5	697.5	40.0	1711	US-11-143-984A-38	Sequence 37, Appl
6	673.5	38.6	1705	US-11-143-984A-37	Sequence 22, Appl
7	635	36.4	1463	US-11-080-991-22	Sequence 22, Appl
8	618.5	35.5	2314	US-11-097-728-2	Sequence 2, Appl
9	618.5	35.5	2353	US-11-097-728-2	Sequence 2, Appl
10	616.5	35.3	1445	US-11-169-041-181	Sequence 181, Appl
11	610	35.0	1452	US-10-821-234-1102	Sequence 1102, Appl
12	586	33.6	647	US-11-000-463-722	Sequence 722, Appl
13	586	33.6	1897	US-10-821-234-1635	Sequence 1635, Appl
14	583.5	33.5	1254	US-10-528-031-47	Sequence 47, Appl
15	545	32.4	570	US-11-143-984A-10	Sequence 14, Appl
16	513	29.4	415	US-10-444-826-14	Sequence 14, Appl
17	513	29.4	415	US-10-444-826-12	Sequence 12, Appl
18	513	29.4	415	US-11-143-984A-206	Sequence 206, Appl
19	513	29.4	415	US-10-444-826-10	Sequence 10, Appl
20	500	28.7	363	US-10-444-826-10	Sequence 8, Appl
21	499	28.4	382	US-10-444-826-10	Sequence 8, Appl
22	496	28.2	339	US-10-509-773-6	Sequence 6, Appl
23	473.5	27.2	426	US-11-197-489-5	Sequence 5, Appl
24	473.5	27.2	426	US-11-197-489-5	Sequence 5, Appl
25	473.5	27.2	463	US-11-197-489-6	Sequence 6, Appl

26	473	27.1	1267	US-11-109-156-35	Sequence 35, Appl
27	449.5	25.8	405	US-11-197-489-7	Sequence 7, Appl
28	448.5	25.7	398	US-10-509-773-10	Sequence 10, Appl
29	439	25.2	657	US-11-109-156-27	Sequence 27, Appl
30	426	24.4	454	US-11-072-512-2092	Sequence 2092, Appl
31	410.5	23.5	1174	US-10-995-861-697	Sequence 697, Appl
32	409.5	23.5	537	US-11-143-984A-29	Sequence 29, Appl
33	405.5	23.3	537	US-11-109-156-28	Sequence 28, Appl
34	404.5	23.2	565	US-11-072-512-2180	Sequence 2180, Appl
35	397	22.8	1015	US-11-169-041-217	Sequence 217, Appl
36	391	13.2	122	US-11-197-489-8	Sequence 8, Appl
37	108	6.2	395	US-10-506-443A-58	Sequence 58, Appl
38	103	5.9	533	US-10-506-443A-23	Sequence 23, Appl
39	103	5.9	551	US-10-506-443A-22	Sequence 22, Appl
40	103	5.9	551	US-11-109-156-36	Sequence 36, Appl
41	102	5.8	607	US-11-143-984A-150	Sequence 150, Appl
42	102	5.8	662	US-11-143-984A-178	Sequence 178, Appl
43	102	5.8	699	US-11-143-984A-177	Sequence 177, Appl
44	102	5.8	747	US-11-143-984A-176	Sequence 176, Appl
45	102	5.8	806	US-11-143-984A-175	Sequence 175, Appl

ALIGNMENTS

RESULT 1
US-11-112-304A-33
Sequence 33, Application US/11112304A
Publication No. US2006002931A1
GENERAL INFORMATION:
APPLICANT: AMGEN, INC.
APPLICANT: AMGEN, INC.
APPLICANT: Smothers, James
APPLICANT: Fambro, William C.
APPLICANT: Kaitiy, Revital
TITLE OF INVENTION: ANTIBODIES OF ANGIOGENESIS INHIBITING DOMAINS OF CD148
FILE REFERENCE: 3447
CURRENT APPLICATION NUMBER: US/11/112,304A
CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/565,159
PRIOR FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/564,885
PRIOR FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/571,566
PRIOR FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: US 60/585,686
PRIOR FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.3
SEQ ID NO 33
LENGTH: 1337
TYPE: PRT
ORGANISM: Homo sapiens
US-11-112-304A-33
Query Match 50.4%; Score 878.5; DB 7; Length 1337;
Best Local Similarity 56.4%; Pred. No. 2.8e-74;
Matches 164; Conservative 56; Mismatches 68; Indels 3;
Gaps 3;
QY KTSCPRIKQFGEFMKLQADSNVLSKEYEBELKDVGRNOCIDIALPENRKNRNNITL 77
DB KKSILIRVNFAYFKQADSNCGFAEVEDLKLWGISOPRYAAELAEIRKRNKNNVVL 1075
QY PYATVTKLSNVDDPCSDIYNASYPNNFRREYIVTQGPLPCTKODFKNVWMEONVN 137
DB PYDISRVKLS-VQHSITDYINANVMPYSHKDFIATQGPLPTLKDFFRWMEKNYA 1134
QY IAWTQCVKRVKCHWYADQDSLYGDLIOMSSSVLPETWIRREFPICEGSDADH 197
DB IIMTKVCEQKRTCEYVWPKQ-ADYGDITVAAMTSEIVLPETWIRDFVKNIGTSESH 1193
QY RLIRHRYWVMDGCVETQSLLQFVTRDYINSPGAGPTVHCSAGVGRCTFTAL 257

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Db      1194 PL-RQFHTSWPDHGVPTDTLLINFRYLWDMKQSPESPFLVHCSAGVGTGTFIAI 1252
Qy      258 DRILQQLDSKDSVDIYGAVHDLRLHRVHVQTECOYVYLHQCVRVLPARK 308
      1253 DRLIYOIENENTVDYGIYDLRLHRVPLMVOTEDQYVFLNQCVLIVRSOK 1303

REST 2
US-11-995-561-851
; Sequence 851, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE OF INVENTION: DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 851
; LENGTH: 1178
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-851

Query Match      50.3%; Score: 876.5; DB 6; Length 1178;
Best Local Similarity 56.6%; Pred. No. 3.7e-74;
Matches 162; Conservative 56; Mismatches 65; Indels 3; Gaps 3;

Qy      23 IKINQFGHFMKLQDSNVYLLSKYEELKDVGRNOSCDIALPENRGHRYNLLPYDAT 82
      862 IRVNFAYAYKKQKQDSNCGFPEYEDLVGISQPKYALELERNRGNRYNVLPLYDIS 921
Db      862 IRVNFAYAYKKQKQDSNCGFPEYEDLVGISQPKYALELERNRGNRYNVLPLYDIS 921
Qy      83 RYKLSNVDDPCSDYINASYIPGNFRREYITOGPPLGKDPKPMVMEQONVHNIWMT 142
      922 RYKLS-VQHTSDVDIINAMVHGHSKOPITGCPPLNDPFRMVMKNYVAILMWT 980
Db      143 OCTGKGVKCDHMYRADDSDIYGDILQMLSESYLEMTPEPFICSEBDLAHRLRH 202
      981 KCVQGRGTKEELWPSKO-ADDYGDITVAMSELVLEMTIRDFVXKIOVSSEHPL-RO 1038
Qy      203 FHYTVPDGHVPTTOSLIQFVTRVDYINNSPGAGFTVYHCSAGVGTGTFIALDRILQ 262
      1039 FHYTVPDGHVPTTDLINFRYLWDMKQSPESPFLVHCSAGVGTGTFIALDRILY 1098
Db      263 QLDSKDSVDIYGAVHDLRLHRVHVQTECOYVYLHQCVRVLPARK 308
      1099 QIENENTVDYGIYDLRLHRVPLMVOTEDQYVFLNQCVLIVRSOK 1144

RESULT 3
US-11-143-984A-28
; Sequence 28, Application US/11143984A
; Publication No. US20060014180A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
; FILE REFERENCE: D0072 DIV1
; CURRENT APPLICATION NUMBER: US/11/143,984A
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/256,868
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/280,186
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/287,735
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US 60/295,848
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/300,465
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 208

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; SOFTWARE: Patentin version 3.2
; SEQ ID NO 28
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-143-984A-28

Query Match      44.0%; Score 768; DB 7; Length 405;
Best Local Similarity 48.9%; Pred. No. 1.4e-64;
Matches 149; Conservative 59; Mismatches 87; Indels 10; Gaps 4;

Qy      2 DPLSLVHNLGKRG--NRKTSCEPIKQFEGHFMKLQDSNVYLLSKYEELKDVGRNOS 58
      83 DYLLAFYINPMSKGLKRRKLTNVOLDPDSYIDWAKSDYKSLQFEEKLIGLDIP 142
Db      59 CDIALPENRGHRYNLLPYDATRYVLSNVDDPCSDYINASYIPGNFRREYITOGP 118
      143 HRAADLPINCKKRYNLLPDPFSRVRLVSMKEEGADYINAVYIPGVNSPOEVIATOGP 202
Qy      119 LGCTDDPMMVMEQONVHNIWMTQCEKGRYKCDHMYRADDSDIYGDILQMLSESYL 178
      203 LPTNDPMMVNLQKSHIYMLTQCNKERRKXCDHYMPTEPIAYGDIIVKVSSEBE 262
Qy      179 PEMTIRFKICGEQDLAHLRLHRYTVPDGHVP--ETTSLOFQVTRVDYINRSPG 236
      263 EDMSKRPRL--NVADAQVMEHNTGMPDGVPPANAESILQFVTRQQAAS-- 317
Db      237 AGFTVHCSAGVGTGTFIALDRILQQLDSKDSVDIYGAVHDLRLHRVHVQTECOYVL 296
      318 KSPMTIRHCSAGVGTGTFIALDRILQIRHDFVDILGLVSEKRSIRMSVOTIEOYIFI 377
Qy      297 HOCVR 301
      378 HOCVR 382

RESULT 4
US-11-143-984A-27
; Sequence 27, Application US/11143984A
; Publication No. US20060014180A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
; FILE REFERENCE: D0072 DIV1
; CURRENT APPLICATION NUMBER: US/11/143,984A
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/256,868
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/280,186
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/287,735
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US 60/295,848
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/300,465
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 27
; LENGTH: 1188
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-11-143-984A-27

Query Match      43.7%; Score 761.5; DB 7; Length 1188;
Best Local Similarity 49.8%; Pred. No. 2.3e-63;
Matches 143; Conservative 56; Mismatches 81; Indels 7; Gaps 3;

Qy      17 RTGSPKIKNQFQGHFMKLQDSNVYLLSKYEELKDVGRNOSCDIALPENRGHRYNLL 76
      884 RLTNPVQDLDPAYIKDMADSDYKFSIQFEEKLIGLDIPRAADPLPFRCCNRYTNI 943
Db      77 LPTNDPMMVNLQKSHIYMLTQCNKERRKXCDHYMPTEPIAYGDIIVKVSSEBE 136

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Db      944  LPDPSRVALYSWNEEGADYINAVINATYNSPOEITATOGLEETENDPMWVNLQKSSQ 1003
      137  NIMWTQCEKGRVYKCDHWYPADQSLYGBLLQMLSSVLPMTREKICGSEQLDA 136
      1004  IIMLTQCEKGRVYKCDHWYPADQSLYGBLLQMLSSVLPMTREKICGSEQLDA 1060
      197  HRLIRHFHYTWPDPHGV-ETTGSLIOFRTVTDYINRSFGAGPTVVCAGVGRGTGTF 254
      1061  MOVWMENTYAMPDHPGPTANNAESILQFVHVRQOATKS--KQPMTHHCSAGVGRGTGTF 1118
      255  IALDRILQOLDSKDSVDIYGAVHDLRLHRVHMVQTECOYVYLHOCV 301
      1119  IALDRILQHIRDHEFVDILGLVSEKRSYMSVMQTEBOYIFIHOCVQ 1165

RESULT 5
US-11-143-984A-38
; Sequence 38, Application US/11143984A
; Publication No. US20060014180A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
; FILE REFERENCE: D0072 DIV1
; CURRENT APPLICATION NUMBER: US/11/143,984A
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/256,868
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/280,186
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/287,735
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US 60/295,848
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/300,465
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1711
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-143-984A-38

Query Match      40.0%; Score 697.5; DB 7; Length 1711;
Best Local Similarity 46.1%; Pred. No. 3,8e-57;
Matches 131; Conservative 59; Mismatches 91; Indels 3; Gaps 2;

      18  KTSCTPKINQEPGFMKQADSNILSKYEELKDYGNOSCDIALPBRGKNNYNTIL 77
      1125  KTRRPPIHSHFROSTKSAHQAQFPFOEBELKEVGKQDPRLEAHPNIIKRRPHVL 1184
      78  PYDATRYKLSNVDDPCSDYINASTYIPGNFRREYIVTQGPLPGTKODPFWKAVWEQNTN 137
      1185  PYDSRVRLTQLPQEPHSDYINANFIPGYSHTOEIATOGPLKKTLEDPMRLWEQOVHV 1244
      138  IYWTQCEKGRVYKCDHWYPADQSLYGBLLQMLSSVLPMTREKICGSEQLDA 196
      1245  IIMLTQCEKGRVYKCDHWYPADQSLYGBLLQMLSSVLPMTREKICGSEQLDA 1302
      197  HRLIRHFHYTWPDPHGV-ETTGSLIOFRTVTDYINRSFGAGPTVVCAGVGRGTGTF 256
      1303  ORRVKQLQFTTWDPHSPVAPPSLLAFVHLYOEVVATOGKGPLVHCSAGVGRGTGTFVA 1362
      257  LDRILQOLDSKDSVDIYGAVHDLRLHRVHMVQTECOYVYLHOCV 300
      1363  LRLRLQLEBEKVADVFNVTYILRLHRPLMIQTLSQYIFLHSC 1406

RESULT 6
US-11-143-984A-37
; Sequence 37, Application US/11143984A
; Publication No. US20060014180A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
; FILE REFERENCE: D0072 DIV1
; CURRENT APPLICATION NUMBER: US/11/143,984A
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/256,868
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/280,186
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/287,735
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US 60/295,848
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/300,465
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 1705
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-143-984A-37

Query Match      38.6%; Score 673.5; DB 7; Length 1705;
Best Local Similarity 45.1%; Pred. No. 6.9e-55;
Matches 128; Conservative 57; Mismatches 96; Indels 3; Gaps 2;

      18  KTSCTPKINQEPGFMKQADSNILSKYEELKDYGNOSCDIALPBRGKNNYNTIL 77
      1125  KTRRPPIHSHFROSTKSAHQAQFPFOEBELKEVGKQDPRLEAHPNIIKRRPHVL 1184
      78  PYDATRYKLSNVDDPCSDYINASTYIPGNFRREYIVTQGPLPGTKODPFWKAVWEQNTN 137
      1185  PYDSRVRLTQLPQEPHSDYINANFIPGYSHTOEIATOGPLKKTLEDPMRLWEQOVHV 1244
      138  IYWTQCEKGRVYKCDHWYPADQSLYGBLLQMLSSVLPMTREKICGSEQLDA 196
      1245  IIMLTQCEKGRVYKCDHWYPADQSLYGBLLQMLSSVLPMTREKICGSEQLDA 1302
      197  HRLIRHFHYTWPDPHGV-ETTGSLIOFRTVTDYINRSFGAGPTVVCAGVGRGTGTF 256
      1303  ORRVKQLQFTTWDPHSPVAPPSLLAFVHLYOEVVATOGKGPLVHCSAGVGRGTGTFVA 1362
      257  LDRILQOLDSKDSVDIYGAVHDLRLHRVHMVQTECOYVYLHOCV 300
      1363  LRLRLQLEBEKVADVFNVTYILRLHRPLMIQTLSQYIFLHSC 1406

RESULT 7
US-11-080-991-22
; Sequence 22, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Velby, Pelter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US-11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 1463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-22

Query Match      36.4%; Score 635; DB 7; Length 1463;
Best Local Similarity 46.4%; Pred. No. 2.3e-51;

```


Matches 130; Conservative 47; Mismatches 93; Indels 10; Gaps 6;

QY 23 IKINQFEGHFMKQADSNYLSKEYEELKDVGRN-OSCDIAL-----LPENGRKRY 73
 DB 891 IIVADILQHTCKMKGCGKFEYELPE-QQTASMTAKENENNRKRGNIISYDS 949
 QY 83 RYKLSNDPDCSDYINASYI PGNPFREYITQGPLGKTDPMWMEONVNIYMT 142
 DB 950 RYKLVLDSPHSDYINNYIDGHRPRHITQPMOETVKDFWMTWQNSASITMT 1009
 QY 143 QCVKGRYKCDHWPPADDSLYGDLILQMSSEVLPETIREFKICEBOLDH--RLI 200
 DB 1010 NIVEGRKCVRWPDTE--YGDIKVTLIETBELAIVIKFTV---QKGYHREL 1064
 QY 201 RHFTYTPHGVPEETOSLIQFRTVRYINRSFGAGFTVWCHSGRGRTIADLI 260
 DB 1065 RLHFTSPHGVPCYATGELGFYRQK-FLN-PEAGPIVWCHSGAGRTCFIADTM 1122
 QY 261 LQQLDSKSDYIYGAVDILRHRYVMQTECOYVYLHOCV 300
 DB 1123 LQMAENEGVVDIFNCVREIRAQRVNLVQTEBOYVFVHDAI 1162

RESULT 8
 US-11-097-728-2
 / Sequence 2, Application US/11097728
 / Publication No. US20050260132A1
 / GENERAL INFORMATION:
 / APPLICANT: Erik Poehr
 / APPLICANT: Sabine Muller
 / APPLICANT: Daniel J. Chin
 / TITLE OF INVENTION: MONOCLONAL ANTIBODIES DIRECTED TO RECEPTOR PROTEIN
 / TITLE OF INVENTION: TYROSINE PHOSPHATASE ZETA
 / FILE REFERENCE: AGYT-006CIP
 / CURRENT APPLICATION NUMBER: US/11/097,728
 / PRIOR FILING DATE: 2005-03-31
 / PRIOR APPLICATION NUMBER: 10/652,981
 / NUMBER OF SEQ ID NOS: 14
 / SOFTWARE: FASTSEQ for Windows Version 4.0
 / SEQ ID NO 2
 / LENGTH: 2314
 / TYPE: PRT
 / ORGANISM: Homo Sapiens
 / US-11-097-728-2

Query Match 35.5%; Score 618.5; DB 7; Length 2314;
 Best Local Similarity 42.2%; Pred. No. 1.5e-49;
 Matches 132; Conservative 54; Mismatches 104; Indels 23; Gaps 8;

QY 23 IKINQFEGHFMKQADSNYLSKEYEELKDVGRN-OSCDIAL-----LPENGRKRY 73
 DB 1698 IPIKHPFHYADLHASSGP--TEFETLKEFQEVQSCVLDGITADSSNHPDKHKNRY 1755
 QY 74 NNLIPYDTRYKLSNV--DDPCSDYINASYI PGNPFREYITQGPLGKTDPMWMEONVNIYMT 131
 DB 1756 INIVAYDSRKYLAQIAEKDGLTDYINNYVDGNRPKAYIAQGFLEKSTAEDEPFRMTW 1815
 QY 132 EQVNIYMTQCVKGRYKCDHWPPADDSLYGDLILQMSSEVLPETIREF----- 186
 DB 1816 ENHVEYIVMTINVEGRKCKDQWPPAD--GSEYGNFLVQKSVQVLAYVIRNFILRNT 1874
 QY 187 --KICEBOLDARHLRHFTYTPHGVPEETOSLIQFRTVRYINRSFGAGFTVWCH 244
 DB 1875 KIKKSGQGRPSGRVVTQYHYTQMPDWGVEPISLVLFYAKKA-YAKH-AVGPVYVHC 1932
 QY 245 SAGVGRGTGTFTALDRILQQLDSKSDYIYGAVDILRHRYVMQTECOYVYLHOCVADVL 304
 DB 1933 SAGVGRGTGTFTALDRILQQLDSKSDYIYGAVDILRHRYVMQTEBOYVFHDITVEAI 1992
 QY 305 PARKLRSEQHNNH 317
 DB 305 PARKLRSEQHNNH 317

DB 1993 LSKETEVLDSHH 2005

RESULT 9
 US-11-097-728-6
 / Sequence 6, Application US/11097728
 / Publication No. US20050260132A1
 / GENERAL INFORMATION:
 / APPLICANT: Erik Poehr
 / APPLICANT: Sabine Muller
 / APPLICANT: Daniel J. Chin
 / TITLE OF INVENTION: MONOCLONAL ANTIBODIES DIRECTED TO RECEPTOR PROTEIN
 / TITLE OF INVENTION: TYROSINE PHOSPHATASE ZETA
 / FILE REFERENCE: AGYT-006CIP
 / CURRENT APPLICATION NUMBER: US/11/097,728
 / PRIOR FILING DATE: 2005-03-31
 / PRIOR APPLICATION NUMBER: 10/652,981
 / NUMBER OF SEQ ID NOS: 14
 / SOFTWARE: FASTSEQ for Windows Version 4.0
 / SEQ ID NO 6
 / LENGTH: 2353
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: VARSPLIC
 / LOCATION: (1)...(2353)
 / OTHER INFORMATION: PTP-zeta SM2 23a exon variant
 / US-11-097-728-6

Query Match 35.5%; Score 618.5; DB 7; Length 2353;
 Best Local Similarity 42.2%; Pred. No. 1.5e-49;
 Matches 133; Conservative 54; Mismatches 104; Indels 23; Gaps 8;

QY 23 IKINQFEGHFMKQADSNYLSKEYEELKDVGRN-OSCDIAL-----LPENGRKRY 73
 DB 1698 IPIKHPFHYADLHASSGP--TEFETLKEFQEVQSCVLDGITADSSNHPDKHKNRY 1755
 QY 74 NNLIPYDTRYKLSNV--DDPCSDYINASYI PGNPFREYITQGPLGKTDPMWMEONVNIYMT 131
 DB 1756 INIVAYDSRKYLAQIAEKDGLTDYINNYVDGNRPKAYIAQGFLEKSTAEDEPFRMTW 1815
 QY 132 EQVNIYMTQCVKGRYKCDHWPPADDSLYGDLILQMSSEVLPETIREF----- 186
 DB 1816 ENHVEYIVMTINVEGRKCKDQWPPAD--GSEYGNFLVQKSVQVLAYVIRNFILRNT 1874
 QY 187 --KICEBOLDARHLRHFTYTPHGVPEETOSLIQFRTVRYINRSFGAGFTVWCH 244
 DB 1875 KIKKSGQGRPSGRVVTQYHYTQMPDWGVEPISLVLFYAKKA-YAKH-AVGPVYVHC 1932
 QY 245 SAGVGRGTGTFTALDRILQQLDSKSDYIYGAVDILRHRYVMQTECOYVYLHOCVADVL 304
 DB 1933 SAGVGRGTGTFTALDRILQQLDSKSDYIYGAVDILRHRYVMQTEBOYVFHDITVEAI 1992
 QY 305 PARKLRSEQHNNH 317
 DB 1993 LSKETEVLDSHH 2005

RESULT 10
 US-11-169-041-181
 / Sequence 181, Application US/11169041
 / Publication No. US20060019284A1
 / GENERAL INFORMATION:
 / APPLICANT: Bristol-Myers Squibb Company
 / TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
 / TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
 / TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
 / FILE REFERENCE: 10001 NP
 / CURRENT APPLICATION NUMBER: US/11/169,041
 / PRIOR FILING DATE: 2005-06-28

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Oy 143 QCEKGRKACDHWPADPOSLVYDGLILQWLEBSVLPFWMTIREFKICEPOLDLH--RLI 200
Db 999 NLVEGRKXCKCKWPDDE--IYDIDVLTIELTBLAEVIIRFAN---EKRGVHEIREI 1053
Oy 201 RHHTYHWPHBQVPEETGSLQFPRTEDYINRSGAGPYNVCSAGYGRGTFILADI 260
Db 1054 RQHTFLGPDGDPYHATGTLQFVKQYS--KSPSAGPLVNCASGAGRGCTGYIDIM 1111
Oy 261 LQOLDSKDSVDYIGAVHDLRHRYVMQTEECQYVYLHCQV 300
Db 1112 LQNAEREGVDIYVCRLEISRNVNMQTEBOYVEIHDAI 1151

RESULT 12
US-11-000-463-722
Sequence 722, Application US/11000463
Publication No. US2005026423A1
GENERAL INFORMATION:
APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Aundi, Vinod
APPLICANT: Chen, Rui-hong
APPLICANT: Qian, Xiaohong B.
APPLICANT: Wang, Zhiwei
APPLICANT: Wehrman, Tom
APPLICANT: Zhang, Jie
APPLICANT: Zhou, Ping
APPLICANT: Cao, Yi-Cheng
APPLICANT: Dmanac, Radoje T.
TITLES OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785C1P4CN
CURRENT APPLICATION NUMBER: US/11/000,463
CURRENT FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: 10/291,265
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/611,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FaetSeq for Windows Version 3.0
SEQ ID NO: 722
LENGTH: 647
TYPE: PRT
ORGANISM: Homo sapiens
US-11-000-463-722

33.6% Score 586, DB 71, Length 647;
Best Local Similarity 42.6%; Pred. NO. 3.1e-47;
Matches 127; Conservative 52; Mismatches 101; Indels 18; Gaps 7;

Oy 22 PIKIOEGHFMKLQADSNYLKSEYEELKVGNRNOSCDIALLENNGKRVNLIPLPA 81
Db 71 PIPIDLADIREELKANGKXKFSQEYESI--DPGQGFTEWNSNLEVNKPKRVANYAIYDH 129
Oy 82 TTVKLSNVDDPCSDIYIAASYIGNNPFRREYIVYQSLPGTCDPFMQVWMEQNVIMV 141
Db 130 SVALTISIDVGSVDYINANYIDGRKQNAVIAIQGLPETIGQFWMWDEORTATVVM 189
Oy 142 TQCEKRVKVCCHWYAPDOOSLYGBDLILQWLESVLPFWMTIREFKICEPOLDLH--RLI 199
Db 190 TLBEKRVKVCQWPA--RGTEGSLIQVTLIDVBLATYVTRFFALHMSGSSE---KRE 245
Oy 200 IHHHTYWDHGVPETTGSLQFPRTYADYINRSP--GAGPLVWNCASGAGRGCTGYID 258

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DB      246 LRQGFPMAMPDHGVPEYPTPLAFIRVAC---NPLDAGPMVHCASGVRTGCFIVD 302
QY      259 RILQOOLDSKSDVYICAVHDLRLHRVHMVQTECOVYVTHO-----CYRDLARAKL 309
DB      303 AMLEBMKHEKTVDIYGHVTCMRSGRMVQTEDQVYFIHEALLLEAATGHTVEPAAKL 360

RESULT 13
US-10-821-234-1635
/ Sequence 1635, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andaman, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pt seq_genes Version 1.0
/ SEQ ID NO: 1635
/ LENGTH: 1897
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-1635

Query Match      33.6%; Score 586; DB 6; Length 1897;
Best Local Similarity 42.6%; Pred. No. 1.3e-46;
Matches 127; Conservative 52; Mismatches 101; Indels 18; Gaps 7;

QY      22 PIKINQFEGHFMKLQADSNVYLSKEYELKDVGRNOSCDIALPENRGKRNINILPYDA 81
DB      1321 PIPITDLADNIERLKANDGLKFSQVEESI-DGQOFTWENSINLEVKRKNYANVAYADH 1379
QY      82 TRYKLSNVDDPCSDYINASYIPGNFRREYIVTGGPLPQTKDDEKMWMEONVHNIWV 141
DB      1380 SSVILTSIDVPCSDYINANYIDGRKONAYIATGGPLPETMGDFRWVWQRTATVVMK 1439
QY      142 TOCVKRGVACHWYMPADQSLVYGLILQMLSESVLPWTIREFKI--CGEOLDARHL 199
DB      1440 TLEBKSRVACDQYMPA-RGTETGGLQVTLDTVELATYVTFALHKSSSE--KRE 1495
QY      200 IRHHVYVWPDHGVPEPTOSLQVPTVTDYINRSP-GAGPTVHCSAGVGRGTGFIAD 258
DB      1496 LRQGFPMAMPDHGVPEYPTPLAFIRVAC---NPLDAGPMVHCASGVRTGCFIVD 1552
QY      259 RILQOOLDSKSDVYICAVHDLRLHRVHMVQTECOVYVTHO-----CYRDLARAKL 309
DB      1553 AMLEBMKHEKTVDIYGHVTCMRSGRMVQTEDQVYFIHEALLLEAATGHTVEPAAKL 1610

RESULT 14
US-11-000-463-250
/ Sequence 250, Application US/11000463
/ Publication No. US2005026423A1
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Qian, Xiaohong B.
/ APPLICANT: Wang, Zhimei
/ APPLICANT: Wehman, Tom
/ APPLICANT: Zhang, Ping
/ APPLICANT: Zhou, Jie
/ APPLICANT: Cao, Yi-Cheng
/ APPLICANT: Dimaec, Radoc's T.
/ TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides

```

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/ FILE REFERENCE: 785CIP4CN
/ CURRENT APPLICATION NUMBER: US/11/000,463
/ CURRENT FILING DATE: 2004-11-29
/ PRIOR APPLICATION NUMBER: 10/291,265
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: PCT/US01/02623
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 09/922,279
/ PRIOR FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: 09/491,404
/ PRIOR FILING DATE: 2000-01-25
/ PRIOR APPLICATION NUMBER: 09/617,746
/ PRIOR FILING DATE: 2000-07-17
/ PRIOR APPLICATION NUMBER: 09/631,451
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: 09/633,870
/ PRIOR FILING DATE: 2000-09-15
/ NUMBER OF SEQ ID NOS: 944
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 250
/ LENGTH: 1907
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-000-463-250

Query Match      33.6%; Score 586; DB 7; Length 1907;
Best Local Similarity 42.6%; Pred. No. 1.3e-46;
Matches 127; Conservative 52; Mismatches 101; Indels 18; Gaps 7;

QY      22 PIKINQFEGHFMKLQADSNVYLSKEYELKDVGRNOSCDIALPENRGKRNINILPYDA 81
DB      1331 PIPITDLADNIERLKANDGLKFSQVEESI-DGQOFTWENSINLEVKRKNYANVAYADH 1389
QY      82 TRYKLSNVDDPCSDYINASYIPGNFRREYIVTGGPLPQTKDDEKMWMEONVHNIWV 141
DB      1390 SSVILTSIDVPCSDYINANYIDGRKONAYIATGGPLPETMGDFRWVWQRTATVVMK 1449
QY      142 TOCVKRGVACHWYMPADQSLVYGLILQMLSESVLPWTIREFKI--CGEOLDARHL 199
DB      1450 TLEBKSRVACDQYMPA-RGTETGGLQVTLDTVELATYVTFALHKSSSE--KRE 1505
QY      200 IRHHVYVWPDHGVPEPTOSLQVPTVTDYINRSP-GAGPTVHCSAGVGRGTGFIAD 258
DB      1506 LRQGFPMAMPDHGVPEYPTPLAFIRVAC---NPLDAGPMVHCASGVRTGCFIVD 1562
QY      259 RILQOOLDSKSDVYICAVHDLRLHRVHMVQTECOVYVTHO-----CYRDLARAKL 309
DB      1563 AMLEBMKHEKTVDIYGHVTCMRSGRMVQTEDQVYFIHEALLLEAATGHTVEPAAKL 1620

RESULT 15
US-10-528-031-47
/ Sequence 47, Application US/10528031
/ Publication No. US20050262577A1
/ GENERAL INFORMATION:
/ APPLICANT: ORIDIS BIOMED Forschungs- und Entwicklungs GmbH
/ APPLICANT: Quelly, Christian
/ APPLICANT: Buck, Charles R.
/ APPLICANT: Zatloukal, Kurt
/ TITLE OF INVENTION: Polypeptides and nucleic acids encoding these and their use for
/ TITLE OF INVENTION: Prevention, diagnosis or treatment of liver disorders and epi-
/ FILE REFERENCE: Oridis Biomed
/ CURRENT APPLICATION NUMBER: US/10/528,031
/ CURRENT FILING DATE: 2005-03-16
/ NUMBER OF SEQ ID NOS: 73
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO: 47
/ LENGTH: 1254
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-10-528-031-47

Query Match      33.5%; Score 583.5; DB 6; Length 1254;

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Best Local Similarity 41.7%; Pred. No. 1.3e-46;
 Matches 118; Conservative 56; Mismatches 104; Indels 5; Gaps 4;

Qy	22	PIKINQFEGHFMKLQADSNYLKSEYEELKDVGNOSCDIALPENRGKRRYNNILPYDA	81
Db	678	PIPIELADHIERLKANDNLKFSQETESI-DPGQFTWEHSNLEVNKPKRRYANVIAYDH	736
Qy	82	TRVYLSNVDDPCSDYINASYIPKNNFRREYITVGGPLPGTMDPFMGMWEONVNIYV	141
Db	737	SRVLSAIEGIFGSDYNNAYIDGRKKNAYIATQSLPETGDFMRMWEQRSATVMM	796
Qy	142	TQCVKGRYKCDHWPPADQSLYGDLLQMLSESVLPENTIREPKICGEQLDAHLIR	201
Db	797	TKLEERSKRVKCDQYTPS-RGTEHGLVOVTLDTVELATYCVRTFALY-KNGSSEKREVR	854
Qy	202	HFHYVWPDHGVPEPTTOSLIQFRTVADYINRSPGAGPTVHCSAGVGTGTFTALDRIL	261
Db	855	QFOFTAMPDHPGVPHPTPFLAFLRRVKTG--NPEDAGPMVHCSAGVGTGCFIVIDAML	912
Qy	262	QQLDSKDSYDIYGAVHDLRLHRVHVQTECOYVYLHCVRDVL	304
Db	913	ERIKHEKTVDIYGHVTLMRQRRNVVQTEDOYIFIDHALLNAV	955

Search completed: February 17, 2006, 01:40:06
 Job time : 19 secs

GenCore version 5.11.7
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OM protein - protein search, using sw model

Run on: February 17, 2006, 01:11:39 / Search time 186 Seconds
(without alignments)
753.558 Million cell updates/sec

Title: US-10-634-027-7
Perfect score: 1744
Sequence: 1 GDRPLSVHLNIGQKGNKRTS.....VRDVLPARKLNSEQHNNH 319

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_21.*

1: geneseqp19808.*
2: geneseqp19808.*
3: geneseqp20018.*
4: geneseqp20018.*
5: geneseqp20028.*
6: geneseqp20038.*
7: geneseqp20038.*
8: geneseqp20048.*
9: geneseqp20058.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1744	100.0	319	8	AD004585 Human HPT
2	1691	97.0	336	8	AD004582 Human HPT
3	1681	97.0	1987	3	AB191974 Human HPT
4	1691	97.0	1987	4	AAW78821 Human HPT
5	1691	97.0	1987	5	AAE20278 Human HPT
6	1691	97.0	1987	7	ABR57179 Human HPT
7	1691	97.0	1987	7	ADJ70328 Human HPT
8	1691	97.0	1987	8	AD004580 Human HPT
9	1691	97.0	2002	4	AAW79805 Human HPT
10	1690	96.9	312	8	AD004584 Human HPT
11	1667	95.6	1450	7	ABR57182 Human HPT
12	1650	94.6	1998	7	AAO24268 Human HPT
13	1644	94.3	579	3	AAH19773 Mouse vas
14	1374	78.8	310	4	AAH78275 Human HPT
15	1367	78.4	254	4	AAH59377 Human HPT
16	878.5	50.4	341	8	ADP74604 Human pro
17	878.5	50.4	1337	2	AAH85203 Human pro
18	878.5	50.4	1337	7	ADL16193 Human pro
19	878.5	50.4	1337	8	ADP74603 Human pro
20	878.5	50.4	1337	8	ADP74603 Human pro
21	878.5	50.4	1337	9	ADY37013 Protein t
22	878.5	50.4	1337	9	ADY37011 Protein t
23	878.5	50.4	1337	9	ADY37133 Protein t
24	868.5	49.6	1216	7	ADL16200 Rat prote

25	868.5	49.8	1238	7	ADL16198	ADL16198 Mouse pro
26	850.5	48.8	1647	4	ABH58428	ABH58428 Drosophila
27	829.5	47.6	1767	4	ABH57126	ABH57126 Drosophila
28	805.5	46.2	1447	7	ABR57181	ABR57181 Drosophila
29	775	44.4	1216	2	AAW10685	AAW10685 Human HPT
30	768	44.0	405	5	ABR52339	ABR52339 Human HPT
31	768	44.0	405	5	ABR52339	ABR52339 Human HPT
32	767	44.0	1217	7	ADH46195	ADH46195 Rat prote
33	767	44.0	1217	7	ADH46195	ADH46195 Rat prote
34	765	43.9	1216	8	ADP54715	ADP54715 Human pro
35	765	43.9	1216	8	ADP24084	ADP24084 PRO poly
36	764	43.8	405	2	AAH85473	AAH85473 Rabbit os
37	761.5	43.7	378	7	ADH46197	ADH46197 Human pro
38	761.5	43.7	1168	2	ADH46197	ADH46197 Human pro
39	761.5	43.7	1168	2	AAW42991	AAW42991 Antio aci
40	761.5	43.7	1168	5	ABR52338	ABR52338 Protein t
41	761.5	43.7	1168	7	ADH46197	ADH46197 Human pro
42	761.5	43.7	1168	8	ADH46197	ADH46197 Human pro
43	760.5	43.6	1187	8	AAW42990	AAW42990 Antio aci
44	744.5	42.7	309	4	AAH78276	AAH78276 Human HPT
45	737.5	42.3	251	4	AAH59378	AAH59378 Drosophila

ALIGNMENTS

RESULT 1

AD004585 standard; protein; 319 AA.

AD004585;

15-JUL-2004 (first entry)

Human HPTbeta catalytic domain.

Protein co-ordinate data: HPTbeta, HPT-beta, PRPB, PRPBeta; PRPB; R-PTP-beta; angiotensin mediated disorder; diabetic retinopathy; sickle cell anaemia; Paget's disease; mycobacterial infection; systemic lupus erythematosus; myopia; Crohn's disease; psoriasis; rheumatoid arthritis; tumour; acquired immune deficiency syndrome; AIDS; drug design; therapy; human.

Homo sapiens.

US2004077065-A1.

22-APR-2004.

04-AUG-2003; 2003US-00634027.

25-SEP-2002; 2002US-0413547P

(PROC) PROCTER & GAMBLE CO.

Evodokimov AG, Pokrosov ME;

WPI; 2004-374235/35.

Identification of compound useful for treatment of angiogenesis mediated disorder, by using three-dimensional structure of HPTbeta catalytic domain, and employing structure to design, or select compound that binds HPTbeta in silico.

Example: SEQ ID NO 7; 315pp; English.

The invention relates to the three dimensional coordinates of HPTbeta (also known as HPT-beta, PRPB, PRPBeta, PRPB or R-PTP-beta) protein. It also relates to a method for the identification of a compound useful for the treatment of an angiogenesis mediated disorder. The compound identified by this method are useful to treat diseases like diabetic retinopathy, sickle cell anaemia, Paget's disease, mycobacterial infections, systemic lupus erythematosus, myopia, Crohn's disease,

PD 25-OCT-2000.
 XX 23-APR-1999; 99EP-00108074.
 XX 23-APR-1999; 99EP-00108074.
 XX (PLAC) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.
 XX Fachinger G, Rissau B, Deutech U;
 XX WPI; 2000-648832/63.
 XX N-PSDB; AAK88866.
 XX Monitoring or modulating Tie-2 tyrosine kinase activity, useful e.g. for
 XX regulating tumor growth, using vascular-endothelial protein tyrosine
 XX phosphatase.
 XX Disclosure; Page 21-27; 60pp; English.
 XX The present sequence is that of human protein tyrosine phosphatase HPRP-
 XX beta, a member of subclases III receptor type PRPs, bearing fibronectin
 XX type III-like repeats in the extracellular domain and a single catalytic
 XX domain in the cytoplasmic tail. HPRP-beta is a vascular-endothelial
 XX protein tyrosine phosphatase (VE-PRP) that specifically interacts with
 XX receptor-tyrosine kinase Tie-2, modulating its tyrosine
 XX phosphorylation. Tie-2 is involved in angiogenic processes, the
 XX formation of blood vessels during embryonal development, wound healing
 XX and in pathological processes such as tumour development. VE-PRPs such as
 XX HPRP-beta or its catalytic domain, nucleic acids and ligands can be used
 XX to monitor, stimulate or repress Tie-2 activity for the purpose of
 XX monitoring or modulating angiogenesis, inducing or inhibiting vascular
 XX growth or remodeling and blood vessel maturation, and inhibiting tumour
 XX growth or metastasis
 XX Sequence 1997 AA;
 SO Query Match 97.0%; Score 1691; DB 3; Length 1997;
 Best Local Similarity 99.4%; Pred. No. 5,6e-179; Indels 0; Gaps 0;
 Matches 312; Conservative 1; Mismatches 1;
 OY 2 DRPLSVHLNIGQGNKRTSCPIKINQPEGHFMKLOADSNYLSKEYEELKQVGNOSCDI 61
 DB 1662 DRPLSVHLNIGQGNKRTSCPIKINQPEGHFMKLOADSNYLSKEYEELKQVGNOSCDI 1721
 OY 62 ALPENRGRKRYNNILPYDARVTLNVDDPCSDYINASYIPGNFRREYIVTQGLPG 121
 DB 1722 ALPENRGRKRYNNILPYDARVTLNVDDPCSDYINASYIPGNFRREYIVTQGLPG 1781
 OY 122 TKDDFMKQWQVQVNIWVWVQCEKGRVYCDHWYPADODSLYYGDLILQMLSSVLPFW 181
 DB 1782 TKDDFMKQWQVQVNIWVWVQCEKGRVYCDHWYPADODSLYYGDLILQMLSSVLPFW 1841
 OY 182 TIREFKICGEBOQDARLIRHFHTVWPDHGVPTTOSLIQFRTVRYINRSPGAPTV 241
 DB 1842 TIREFKICGEBOQDARLIRHFHTVWPDHGVPTTOSLIQFRTVRYINRSPGAPTV 1901
 OY 242 VHCAGVGRGTGFIADRIILQOOLDSKDSVDIYGAVHDLRLHFWVQTECOYYVLIHQVR 301
 DB 1902 VHCAGVGRGTGFIADRIILQOOLDSKDSVDIYGAVHDLRLHFWVQTECOYYVLIHQVR 1961
 OY 302 DVLARARLRSEQH 315
 DB 1962 DVLARARLRSEQH 1975
 RESULT 4
 AAM78821
 ID AAM78821 standard; protein; 1997 AA.
 XX AAM78821;
 XX 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 1483.
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 XX vaccine; peptide therapy; stem cell growth factor; hematopoiesis;
 XX tissue growth factor; immunomodulatory; cancer; leukemia;
 XX nervous system disorder; arthritis; inflammation.
 XX Homo sapiens.
 XX WO200157190-A2.
 XX 09-AUG-2001.
 XX 05-FEB-2001; 2001MO-US004098.
 XX 03-FEB-2000; 2000US-00495914.
 XX 27-APR-2000; 2000US-00560875.
 XX 20-UN-2000; 2000US-00560875.
 XX 19-UN-2000; 2000US-00620325.
 XX 01-SEP-2000; 2000US-00654936.
 XX 15-SEP-2000; 2000US-00653561.
 XX 20-OCT-2000; 2000US-00693325.
 XX 30-NOV-2000; 2000US-00728422.
 XX (HYSB-) HYSBQ INC.
 XX Tang YT, Liu C, Dymnac RT, Aundt V, Zhou P, Xu C, Cao Y,
 XX Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX WPI; 2001-476283/51.
 XX N-PSDB; AAK51954.
 XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
 XX in diagnosis and gene therapy.
 XX Claim 20; Page 3761-3764; 6221pp; English.
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 XX encoded polypeptides (AAM78123-AA80302) that exhibit activity relating to
 XX cytokine, cell proliferation or cell differentiation or which may induce
 XX production of other cytokines in other cell populations. The
 XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
 XX peptide therapy. The polypeptides have various cytokine-like activities,
 XX e.g. stem cell growth factor activity, hematopoiesis regulating
 XX activity, tissue growth factor activity, immunomodulatory activity and
 XX activin/inhibin activity and may be useful in the diagnosis and/or
 XX treatment of cancer, leukemia, nervous system disorders, arthritis and
 XX inflammation. Notes: Records for SEQ ID NO 2110 (AAK52581), 2111
 XX (AAK52582) and 3666 (AAM80920) are omitted as the relevant pages from the
 XX sequence listing were missing at the time of publication
 SO Sequence 1997 AA;
 Query Match 97.0%; Score 1691; DB 4; Length 1997;
 Best Local Similarity 99.4%; Pred. No. 5,6e-179; Indels 0; Gaps 0;
 Matches 312; Conservative 1; Mismatches 1;
 OY 2 DRPLSVHLNIGQGNKRTSCPIKINQPEGHFMKLOADSNYLSKEYEELKQVGNOSCDI 61
 DB 1662 DRPLSVHLNIGQGNKRTSCPIKINQPEGHFMKLOADSNYLSKEYEELKQVGNOSCDI 1721
 OY 62 ALPENRGRKRYNNILPYDARVTLNVDDPCSDYINASYIPGNFRREYIVTQGLPG 121
 DB 1722 ALPENRGRKRYNNILPYDARVTLNVDDPCSDYINASYIPGNFRREYIVTQGLPG 1781
 OY 122 TKDDFMKQWQVQVNIWVWVQCEKGRVYCDHWYPADODSLYYGDLILQMLSSVLPFW 181
 DB 1782 TKDDFMKQWQVQVNIWVWVQCEKGRVYCDHWYPADODSLYYGDLILQMLSSVLPFW 1841
 OY 182 TIREFKICGEBOQDARLIRHFHTVWPDHGVPTTOSLIQFRTVRYINRSPGAPTV 241
 DB 1842 TIREFKICGEBOQDARLIRHFHTVWPDHGVPTTOSLIQFRTVRYINRSPGAPTV 1901

immunomodulator; gene therapy; metabolic disease; eating disorder;
 body weight regulation disorder; cachexia; diabetes mellitus; cancer;
 hypertension; coronary heart disease; hypercholesterolaemia; gallstone;
 dyslipidaemia; osteoarthritis; sleep apnea; human; chromosome 12;
 protein tyrosine phosphatase receptor type B precursor; PTPRB.

XX Homo sapiens.
 XX MO2003047611-A2.
 XX 12-JUN-2003.
 XX 04-DEC-2002; 2002WC-EP013744.
 XX 04-DEC-2001; 2001EP-00128844.
 XX 07-DEC-2001; 2001EP-00129138.
 XX 07-JUN-2002; 2002EP-00000010.
 XX (DEVE-) DEVELOPGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
 XX Meise M, Eulenbergh K, Fritsch R, Haeder T, Broemner G;
 F1 Steuernagel A;
 XX WPI; 2003-532801/50.
 XX N-PSDB; ACC79776.
 XX New compositions comprising tyrosine phosphatase PTP10D, protein tyrosine
 PT kinase Tec or egg-derived tyrosine phosphatase genes or proteins, useful
 PT for treating or preventing metabolic diseases, e.g. as obesity or
 PT cachexia.
 XX Claim 2, Fig. 8b; 83pp; English.
 XX The present invention describes a pharmaceutical composition comprising a
 CC nucleic acid (i) protein tyrosine phosphatase PTP10D, non-receptor
 CC protein tyrosine kinase Tec, egg derived tyrosine phosphatase (EDTP) gene
 CC family or encoded polypeptide, fragment or variant of nucleic acid
 CC molecule or polypeptide, an antibody, an aptamer or receptor recognising
 CC a nucleic acid molecule of PTP10D, Tec, or EDTP gene family or encoded
 CC polypeptide, and a carrier, diluent and/or adjuvant. The pharmaceutical
 CC composition can have antidiabetic, hypotensive, cardiac, antihypertensive,
 CC osteoporotic, cytoostatic, anorectic, and immunomodulator activities, and
 CC can be used in gene therapy. The composition is useful for the
 CC manufacture of an agent for detecting and/or verifying, for treating and
 CC alleviating and/or preventing a disorder, including metabolic diseases
 CC such as obesity and other body weight regulation disorders, as well as
 CC related disorders such as eating disorder, cachexia, diabetes mellitus,
 CC hypertension, coronary heart disease, hypercholesterolaemia,
 CC dyslipidaemia, osteoarthritis, gallstones, cancers (cancers of the
 CC reproductive organ), sleep apnea, and other diseases, in cells, cell
 CC masses, organs and/or subjects. The components of the composition may
 CC also be used in controlling the function of a gene and/or gene product
 CC which is influenced and/or modified by a PTP10D, Tec, or EDTP homologous
 CC polypeptide, and for identifying substances capable of interacting with a
 CC PTP10D, Tec, or EDTP homologous polypeptide. The nucleic acid molecule of
 CC PTP10D, Tec, or EDTP family or their fragments, may be used in the
 CC preparation of a non-human animal which over- or under-expresses the
 CC PTP10D, Tec, or EDTP gene product. The present sequence represents human
 CC protein tyrosine phosphatase receptor type B precursor (PTPRB), which is
 CC a human PTP10B homologous sequence. Human PTPRB is located to chromosome
 CC 12
 CC XX
 SQ Sequence 1997 AA;
 Query Match 97.0%; Score 1691; DB 7; Length 1997;
 Best Local Similarity 99.4%; Pred. No. 3,66-179;
 Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DRPLSVHLNKGKGRKTSCTPIKINQFEGHMKLQADSNYLSKEYELKQVGRNSCDI 61
 DB 1662 DRPLSVHLNKGKGRKTSCTPIKINQFEGHMKLQADSNYLSKEYELKQVGRNSCDI 1721
 QY 62 ALPEBNGKRRYNNILPYDARVGLSNVDDPCSDYINASYIPGNFRREYIVQGPPLG 121

DB 1722 ALPEBNGKRRYNNILPYDARVGLSNVDDPCSDYINASYIPGNFRREYIVQGPPLG 1781
 QY 122 TDQDDPKWMEQVNHVITWQCVKGRKCDHPADQDLSYGGDLILQVLSGVLPFM 181
 DB 1782 TDQDDPKWMEQVNHVITWQCVKGRKCDHPADQDLSYGGDLILQVLSGVLPFM 1841
 QY 182 TTRFPCGSGQDARLIRHFHTWTPHGVETTSLLQPRATRYNRSFGAPV 241
 DB 1842 TTRFPCGSGQDARLIRHFHTWTPHGVETTSLLQPRATRYNRSFGAPV 1901
 QY 242 VHCASGVRGTFTIALDRILQDLSQSDVIYGAVDRLRHVHWQTECQYVILHQCVR 301
 DB 1902 VHCASGVRGTFTIALDRILQDLSQSDVIYGAVDRLRHVHWQTECQYVILHQCVR 1961
 QY 302 DVLARKLRSEQHN 315
 DB 1962 DVLARKLRSEQHN 1975

RESULT 7
 ADJ70329
 ID ADJ70329 standard; protein; 1997 AA.
 XX ADJ70329;
 XX 06-MAY-2004 (first entry)
 DT Human heart mitochondrial protein as a therapeutic target SeqID2135.
 XX Human heart mitochondrial protein as a therapeutic target SeqID2135.
 XX Mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteoporotic; ophthalmological; cytoostatic.
 XX Homo sapiens.
 XX MO2003087768-A2.
 XX 23-OCT-2003.
 XX 04-APR-2003; 2003WC-US010870.
 XX 12-APR-2002; 2002US-0372843P.
 XX 17-JUN-2002; 2002US-0386987P.
 XX 20-SEP-2002; 2002US-0412418P.
 XX (MITO-) MITOKOR.
 XX (BUCK-) BUCK INST AGE RES.
 XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
 PI Warnock DE;
 XX WPI; 2003-845369/78.
 XX Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function;
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX Claim 1; SEQ ID NO 2135; 180pp; English.
 CC This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,

PF 05-FEB-2001; 2001WO-US004098.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.
 XX
 PA (HUSE-) HUSEQ INC.
 XX
 PI Tang YT, Liu C, Dmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao Qa, Wang D, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejman T, Goodrich R;
 XX
 DR MPI; 2001-476283/51.
 DR N-PSDB; AAK52938.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 in diagnosis and gene therapy.
 XX
 PS Claim 20; Page 340-341; 6221pp; English.
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAK78323-AAK80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The vaccines or
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAK80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 SQ Sequence 2002 AA:
 Query Match 97.0%; Score 1691; DB 4; Length 2002;
 Best Local Similarity 99.4%; Pred. No. 5, 6e-179;
 Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 DRPLSVHNLGQKNRRTSCPIKINQEGHFMKLDQDSNYLLSKYEELKDVGRNOSCDI 61
 DB 1667 DRPLSVHNLGQKNRRTSCPIKINQEGHFMKLDQDSNYLLSKYEELKDVGRNOSCDI 1726
 QY 62 ALLENKGRKNNIIPYDTRVKLSNVDDPCSDYINASTIPGNFRREYIVTQGPLG 121
 DB 1727 ALLENKGRKNNIIPYDTRVKLSNVDDPCSDYINASTIPGNFRREYIVTQGPLG 1786
 QY 122 TDDFMKQWVQWVNIWVVTQCEKGRVCDHYWPAQDLSLYGDLIQMLSESVLPBW 181
 DB 1787 TDDFMKQWVQWVNIWVVTQCEKGRVCDHYWPAQDLSLYGDLIQMLSESVLPBW 1846
 QY 182 TIREFKIGESQDLARHLIRHFHYTVPDHYGVEPTTOSLQFVTRVDYINRSPGAPTV 241
 DB 1847 TIREFKIGESQDLARHLIRHFHYTVPDHYGVEPTTOSLQFVTRVDYINRSPGAPTV 1906
 QY 242 VCSGSGVGRGTFTALDRILQOLDSKDSVIVGAVHDLFLHRVHMVQSCQVYLHCVR 301
 DB 1907 VCSGSGVGRGTFTALDRILQOLDSKDSVIVGAVHDLFLHRVHMVQSCQVYLHCVR 1966
 QY 302 DTLARKKISEQHH 315
 DB 1967 DTLARKKISEQHH 1980

RESULT 10
 ADO04584
 ID ADO04584 standard; protein; 312 AA.

XX ADO04584;
 AC
 XX 15-JUL-2004 (first entry)
 DT
 XX Human HTPbeta truncated intracellular domain (ICD) protein.
 XX
 DE Protein co-ordinate data; HTPbeta; HTP-beta; PTPB; PTPbeta; PTPB;
 XX R-PTP-beta; angiogenesis mediated disorder; diabetic retinopathy;
 XX sickle cell anemia; Paget's disease; mycobacterial infection;
 XX systemic lupus erythematosus; myopia; Crohn's disease; psoriasis;
 XX rheumatoid arthritis; tumour; acquired immune deficiency syndrome; AIDS;
 XX drug designing; therapy; human; intracellular domain; ICD; mutant;
 XX mutant.
 XX Homo sapiens.
 OS Synthetic.
 XX
 PN US2004077065-A1.
 PD
 XX 22-APR-2004.
 PF
 XX 04-AUG-2003; 2003US-00634027.
 XX
 PR 25-SEP-2002; 2002US-0413547P.
 XX
 XX (PROC) PROCTER & GAMBLE CO.
 XX
 PI Bvdokimov AG, Pokros ME;
 XX
 DR MPI; 2004-374235/35.
 DR N-PSDB; ADO04583.
 XX
 FT Identification of compound useful for treatment of angiogenesis mediated
 FT disorder, by using three-dimensional structure of HTPbeta catalytic
 FT domain, and employing structure to design, or select compound that binds
 FT HTPbeta in silico.
 PT
 XX
 PS Disclosure; SEQ ID NO 6; 335pp; English.
 XX
 CC The invention relates to the three dimensional coordinates of HTPbeta
 CC (also known as HTP-beta, PTPB, PTPbeta, PRP or R-PTP-beta) protein. It
 CC also relates to a method for the identification of a compound useful for
 CC the treatment of an angiogenesis mediated disorder. The compounds
 CC identified by this method are useful to treat diseases like diabetic
 CC retinopathy, sickle cell anaemia, Paget's disease, mycobacterial
 CC infections, systemic lupus erythematosus, myopia, Crohn's disease,
 CC psoriasis, rheumatoid arthritis, solid or blood borne tumours and
 CC acquired immune deficiency syndrome (AIDS). The invention is useful for
 CC the treatment of an angiogenesis mediated disorder or disease. It is also
 CC useful in drug design techniques. The present sequence is human HTPbeta
 CC intracellular domain (ICD) truncated protein.
 XX
 SQ Sequence 312 AA:
 Query Match 96.9%; Score 1690; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 3, 9e-180;
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DRPLSVHNLGQKNRRTSCPIKINQEGHFMKLDQDSNYLLSKYEELKDVGRNOSCDI 61
 DB 1 DRPLSVHNLGQKNRRTSCPIKINQEGHFMKLDQDSNYLLSKYEELKDVGRNOSCDI 60
 QY 62 ALLENKGRKNNIIPYDTRVKLSNVDDPCSDYINASTIPGNFRREYIVTQGPLG 121
 DB 61 ALLENKGRKNNIIPYDTRVKLSNVDDPCSDYINASTIPGNFRREYIVTQGPLG 120
 QY 122 TDDFMKQWVQWVNIWVVTQCEKGRVCDHYWPAQDLSLYGDLIQMLSESVLPBW 181
 DB 121 TDDFMKQWVQWVNIWVVTQCEKGRVCDHYWPAQDLSLYGDLIQMLSESVLPBW 180
 QY 182 TIREFKIGESQDLARHLIRHFHYTVPDHYGVEPTTOSLQFVTRVDYINRSPGAPTV 241

PT Use of the polypeptide comprising vascular endothelial-protein tyrosine
 PT phosphatase (VE-PTP) or the nucleic acid encoding the polypeptide for the
 PT manufacture of an agent for monitoring or modulating VE-cadherin mediated
 PT disorders.
 XX
 XX Example: Fig 2; Opp; English.
 PS
 CC The present invention relates to a polypeptide comprising vascular
 CC endothelial-protein tyrosine phosphatase (VE-PTP) or its active fragment
 CC or effector, or the nucleic acid encoding the polypeptide or its
 CC effector, for use in the manufacture of an agent for monitoring or
 CC modulating VE-cadherin mediated processes or disorders. The polypeptide
 CC comprising vascular endothelial-protein tyrosine phosphatase (VE-PTP) or
 CC its active fragment or effector, or the nucleic acid encoding the
 CC polypeptide or its effector, is useful for the manufacture of an agent
 CC for monitoring or modulating VE-cadherin mediated processes or disorders,
 CC e.g., cancer. The present sequence is a protein shown in the
 CC exemplification of the invention
 XX
 SQ Sequence 1998 AA;
 Query Match 94.6%; Score 1650; DB 7; Length 1998;
 Best Local Similarity 95.9%; Pred. No. 2.2e-174;
 Matches 301; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
 QY 2 DRPLSVHLNIGQKGRKRTSCPIKINQFEGHFMKLDQNSVLLSKYEELNDVGRNQCSDI 61
 DB 1663 DRPLSVHLNIGQKGRKRTSCPIKINQFEGHFMKLDQNSVLLSKYEELNDVGRNQCSDI 1722
 QY 62 ALLEPNNGKRRYNNILPYDAIRVKSNDVDDPCSDYINASYIPGNFRREYIVTQGPLPG 121
 DB 1723 ALLEPNNGKRRYNNILPYDAIRVKSNDVDDPCSDYINASYIPGNFRREYIVTQGPLPG 1782
 QY 122 TKDFFWMAWEDONVNIWVTOCEKGRVKCDHYWADDDPLYVGDYLQWVSESYLPEW 181
 DB 1783 TKDFFWMAWEDONVNIWVTOCEKGRVKCDHYWADDDPLYVGDYLQWVSESYLPEW 1842
 QY 182 TIREFKICEBOLDHRLIRHFYTWDPHGVPETQSLIQFRTVDYINRSPGAGPTV 241
 DB 1843 TIREFKICEBOLDHRLIRHFYTWDPHGVPETQSLIQFRTVDYINRSPGAGPTV 1902
 QY 242 VHCASGVGTGFIALDRILIQOLDSKDSVDIYGAVHDLRLHVRVWVOTECQVYVYHQCVR 301
 DB 1903 VHCASGVGTGFIALDRILIQOLDSKDSVDIYGAVHDLRLHVRVWVOTECQVYVYHQCVR 1962
 QY 302 DVLRARAKRSRQNH 315
 DB 1963 DVLRARAKRSRQNH 1976
 Db
 RESULT 13
 AAB19773
 ID AAB19773 standard; protein; 579 AA.
 XX
 AC AAB19773;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 XX Mouse vascular-endothelial protein tyrosine phosphatase.
 XX
 KM Vascular-endothelial protein tyrosine phosphatase; VE-PTP; mouse; Tie-2;
 KM receptor-type tyrosine kinase; antiangiogenic; antitumor;
 KM antimetastatic; tumour; metastasis; angiogenesis; therapy.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Domain 3..24 "membrane proximal fibronectin II domain"
 FT Domain 204..223 "note="transmembrane domain"
 FT Domain 304..549 "note="catalytic domain"

XX
 XX EPI046715-A1.
 XX
 PD 25-OCT-2000.
 XX
 PF 23-APR-1999; 99EP-00108074.
 XX
 PR 23-APR-1999; 99EP-00108074.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Fachinger G, Rieau B, Deutsch U;
 XX
 DR WPI: 2000-648932/63.
 DR N-PSDB: AAA88865.
 XX
 PT Monitoring or modulating Tie-2 tyrosine kinase activity, useful e.g. for
 PT regulating tumor growth, using vascular-endothelial protein tyrosine
 PT phosphatase.
 XX
 PS Disclosure; Page 10-12; 60pp; English.
 CC
 CC The present sequence is that of murine vascular-endothelial protein
 CC tyrosine phosphatase (VE-PTP). VE-PTP is a member of subclass III
 CC receptor type PTPs, bearing fibronectin type III-like repeats in the
 CC extracellular domain and a single catalytic domain in the cytoplasmic
 CC tail. VE-PTP specifically interacts with receptor-type tyrosine kinase
 CC Tie-2, modulating its tyrosine phosphorylation. Tie-2 is involved in
 CC angiogenic processes, the formation of blood vessels during embryonal
 CC development, wound healing and in pathological processes such as tumour
 CC can be used to monitor, stimulate or repress Tie-2 activity for the
 CC purpose of monitoring or modulating angiogenesis, inducing or inhibiting
 CC vascular growth or remodelling and blood vessel maturation, and
 CC inhibiting tumour growth and metastasis
 XX
 SQ Sequence 579 AA;
 Query Match 94.3%; Score 1644; DB 3; Length 579;
 Best Local Similarity 95.5%; Pred. No. 1.5e-174;
 Matches 300; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
 QY 2 DRPLSVHLNIGQKGRKRTSCPIKINQFEGHFMKLDQNSVLLSKYEELNDVGRNQCSDI 61
 DB 244 DRPLSVHLNIGQKGRKRTSCPIKINQFEGHFMKLDQNSVLLSKYEELNDVGRNQCSDI 303
 QY 62 ALLEPNNGKRRYNNILPYDAIRVKSNDVDDPCSDYINASYIPGNFRREYIVTQGPLPG 121
 DB 304 ALLEPNNGKRRYNNILPYDAIRVKSNDVDDPCSDYINASYIPGNFRREYIVTQGPLPG 363
 QY 122 TKDFFWMAWEDONVNIWVTOCEKGRVKCDHYWADDDPLYVGDYLQWVSESYLPEW 181
 DB 364 TKDFFWMAWEDONVNIWVTOCEKGRVKCDHYWADDDPLYVGDYLQWVSESYLPEW 423
 QY 182 TIREFKICEBOLDHRLIRHFYTWDPHGVPETQSLIQFRTVDYINRSPGAGPTV 241
 DB 424 TIREFKICEBOLDHRLIRHFYTWDPHGVPETQSLIQFRTVDYINRSPGAGPTV 483
 QY 242 VHCASGVGTGFIALDRILIQOLDSKDSVDIYGAVHDLRLHVRVWVOTECQVYVYHQCVR 301
 DB 484 VHCASGVGTGFIALDRILIQOLDSKDSVDIYGAVHDLRLHVRVWVOTECQVYVYHQCVR 543
 QY 302 DVLRARAKRSRQNH 315
 DB 544 DVLRARAKRSRQNH 557
 Db
 RESULT 14
 AAG78275
 ID AAG78275 standard; protein; 310 AA.
 XX
 AC AAG78275;
 XX

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 17, 2006, 01:21:14 ; Search time 41 Seconds

(without alignments)
748.613 Million cell updates/sec

Title: US-10-634-027-7

Perfect score: 1744

Sequence: 1 GRRPLSVHNLGKGRKTS.....VRDVLARKLNSROHHHHH 319

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 28346 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1691	97.0	1997	1 S12050	protein-tyrosine-p
2	1613	92.6	583	2 S17671	protein-tyrosine-p
3	876.5	50.4	1337	1 S13670	protein-tyrosine-p
4	866.5	49.8	1336	2 S68700	HRP beta-like tyr
5	847.5	48.6	1357	2 D41214	protein-tyrosine-p
6	847.5	48.6	1630	2 C41214	protein-tyrosine-p
7	818.5	46.9	1615	2 B49502	protein-tyrosine-p
8	818.5	46.9	1767	2 A49502	protein-tyrosine-p
9	775	44.4	1216	2 S60613	protein-tyrosine-p
10	768	44.0	405	2 S68250	protein-tyrosine-p
11	764	43.8	405	2 S68250	protein-tyrosine-p
12	764	43.8	1226	2 UC7503	protein-tyrosine-p
13	761.5	43.7	1188	1 A57064	protein-tyrosine-p
14	760.5	43.6	1187	1 A57064	protein-tyrosine-p
15	709.5	40.7	1118	1 A53661	protein-tyrosine-p
16	701	40.2	1367	2 T21913	hyphothetical prote
17	697.5	40.0	1111	1 A55148	protein-tyrosine-p
18	675	38.7	2302	2 T14328	protein-tyrosine-p
19	618.5	35.5	2314	1 A46151	protein-tyrosine-p
20	615.5	35.3	1445	1 A48148	protein-tyrosine-p
21	610	35.0	1452	1 S17669	protein-tyrosine-p
22	609	34.9	1452	1 T19121	probable protein-t
23	604.5	34.7	1442	1 B48148	protein-tyrosine-p
24	604.5	34.7	1442	1 S17670	protein-tyrosine-p
25	600.5	34.4	1422	2 T42636	protein-tyrosine-p
26	592.5	34.0	1462	1 B48758	protein-tyrosine-p
27	592.5	34.0	1462	1 A48758	protein-tyrosine-p
28	592.5	34.0	1501	2 S18148	protein-tyrosine-p
29	592.5	34.0	1663	2 S46217	protein-tyrosine-p

30	592	33.9	1290	2 A56493	leucocyte common a
31	591.5	33.9	1907	2 S50893	protein-tyrosine-p
32	590	33.8	1457	1 A48066	protein-tyrosine-p
33	589	33.8	796	1 JC1285	protein-tyrosine-p
34	589	33.8	802	1 A36065	protein-tyrosine-p
35	589	33.8	1440	2 UC6312	protein-tyrosine-p
36	588	33.7	1898	2 S46216	protein-tyrosine-p
37	587.5	33.7	832	2 UC8051	leukocyte antigen-
38	586.5	33.6	1301	1 A41622	protein-tyrosine-p
39	586	33.6	1897	1 TDHLLK	protein-tyrosine-p
40	583.5	33.5	1912	2 A56178	leukocyte antigen-
41	582.5	33.5	1437	2 T31093	protein-tyrosine-p
42	581	33.4	582	2 A57068	probable protein-t
43	580.5	33.3	1459	2 T50212	protein-tyrosine-p
44	578.5	33.2	2029	1 TDFELK	protein-tyrosine-p
45	577.5	33.1	1691	1 D54689	protein-tyrosine-p

ALIGNMENTS

RESULT 1

S12050 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type beta precursor - human

C.Species: Homo sapiens (man)

C.Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004

C.Accession: S12050; S15818; S15819

R.Krueger, N.X.; Streuli, M.; Saito, H.

EMBO J 9, 3241-3252, 1990

A.Title: Structural diversity and evolution of human receptor-like protein tyrosine phk

A.Reference number: S12049; MUID:91006018; PMID:2170109

A.Accession: S12050

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-1997 <KRU>

A.Cross-References: UNIPROT: P23467; UNIPARC: UP10000034765; GB: X54131; NID: g35787; PIDN: RDe Vries, L.; Li, R.Y.; Ragab, A.; Ragab-Thomas, J.M.F.; Chap, H.

FEBS Lett. 282, 285-288, 1991

A>Title: Expression of a truncated protein-tyrosine phosphatase mRNA in human lung.

A.Reference number: S15818; MUID:91243813; PMID:1645282

A.Accession: S15818

A.Status: not compared with conceptual translation

A.Molecule type: mRNA

A.Residues: 1872-1911, 'VHMYLQK' <VRI>

A.Cross-References: UNIPARC: UP10000173861

A.Accession: S15819

A.Status: not compared with conceptual translation

A.Molecule type: mRNA

A.Residues: 1872-1997 <VR2>

A.Cross-References: UNIPARC: UP10000173861

C.Genetics:

A.Gene: GDB: PRPB, PRPB

A.Cross-References: GDB: 127352; OMIM: 176882

A.Map position: 12q13-14q22

C.Keywords: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III ;

F./1-22/Domain: signal sequence #status predicted <SIG>

F./3-1397/Product: protein-tyrosine-phosphatase, receptor type beta #status predicted <

F./1-1625/Domain: extracellular #status predicted <EXT>

F./1626-1642/Domain: transmembrane #status predicted <TM>

F./1643-1997/Domain: intracellular #status predicted <INT>

F./1727-1953/Domain: protein-tyrosine-phosphatase homology <PRP>

F./1904/Active site: Cys (phosphocysteine intermediate) #status predicted

F./1910/Binding site: substrate phosphate (Arg) #status predicted

Query Match 97.0%; Score 1691; DB 1; Length 1997;

Best Local Similarity 99.4%; Pred. No. 3e-137;

Matches 312; Conservative 1; Mismatches 1; Gaps 0;

DB 2 DBPLSVHNLGKGRKTSCKIKNOFEGHFKQLADSNVLSKEYEELKQVGNOSCDI 61
1662 DBPLSVHNLGKGRKTSCKIKNOFEGHFKQLADSNVLSKEYEELKQVGNOSCDI 1721

F/30-818/Domain: extracellular #status predicted <EXT>
 F/30-115/Domain: fibronectin type III repeat homology #status atypical <FN3A>
 F/116-209/Domain: fibronectin type III repeat homology #status atypical <FN3B>
 F/328-415/Domain: fibronectin type III repeat homology <FN3>
 F/431-519/Domain: fibronectin type III repeat homology <FN3B>
 F/528-625/Domain: fibronectin type III repeat homology <FN3>
 F/630-713/Domain: fibronectin type III repeat homology <FN3G>
 F/721-810/Domain: fibronectin type III repeat homology <FN3>
 F/811-1187/Domain: fibronectin type III repeat homology <FN3>
 F/811-875, 876-1187/Domain: fibronectin type III repeat homology <FN3>
 F/813-843/Domain: fibronectin type III repeat homology <FN3>
 F/843-1187/Domain: fibronectin type III repeat homology <FN3>
 F/901-1187/Domain: fibronectin type III repeat homology <FN3>
 F/933-1155/Domain: fibronectin type III repeat homology <FN3>
 F/735,154,189,201,227,277,286,323,369,460,489,699,711,732,789/Binding site: carbohydrate
 F/1107/Active site: Cys (phosphocysteine intermediate) #status predicted
 F/1113/Binding site: substrate phosphate (Arg) #status predicted

Query Match 43.6%; Score 760.5; DB 1; Length 1187;
 Best Local Similarity 49.8%; Pred. No. 3.3e-57;
 Matches 143; Conservative 56; Mismatches 81; Indels 7; Gaps 3;

17 RTSCPIKINQFGHFKLQADSNVLSKEYELKDVGRNQCIDLLENRGNRYNI 76
 DB RLTLNTPVQLDDPAYIKOMADSDYKSLQFELTLGLDIPRADLPRLRCNRYNI 942
 77 LEYATVTKSNVDDPCSDYINASYIPGNFRREYITQGPLFGTKDPFWMVEQNVH 136
 DB LYPDSEKRLSKNEBEGADYINNYIPGNRPQYITQGPLFETRNDPFWVLQCKSQ 1002
 137 NIVWVTCVKEGVKDKHWPADDSLYYDGLLQMLSESVLEWTEPFKICEBOLA 196
 DB 1003 KIVWLTQCNKRRKCDHWPTEPAINADYIVNLSSEEDQDMHNRKFI--NYAE 1059
 197 HELIRHPIYTPDHPGP--ETTSGLIQFRTVDYINRSPAGPTVVCAGVGRGTGP 254
 DB 1060 WODVNHFRYTPADHPGVPFANAASTILQFVHNRQATKS--GEPITHCAGVGRGTGP 1117
 255 IALDRILQQLDSKDSVDYIGAVHDLRLHVMVQTECOVYLLHQCVR 301
 DB 1118 IALDRILQHLRHEFVDILGLVSEMSYSRMSVQTEBOYIFIHQCVO 1164

RESULT 15

A49724
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type H precursor - human
 NAlternate names: protein-tyrosine-phosphatase, stomach cancer-associated type 1, SAP-1
 CSpecies: Homo sapiens (man)
 CDate: 03-May-1994 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
 CAccession: A49724
 RMatosaki, T.; Suzuki, T.; Uchida, T.; Inazawa, J.; Ariyama, T.; Matsuda, K.; Horita, K.
 J. Biol. Chem. 269, 2075-2081, 1994
 ATitle: Molecular cloning of a human transmembrane-type protein tyrosine phosphatase ar
 AReference number: A49724; WUID:94124561; PMID:8294455
 AAccession: A49724
 A.Molecule type: mRNA
 A.Residues: 1-1118 <MATO>
 A.Cross-references: UNIPROT:Q15426; UNIPARC:UPI0000073BF2; GB:D15049; NID:9475003; PIND:
 C.Genetics:
 A.Gene: GDB:PTPH; SAP-1
 A.Cross-references: GDB:305504
 A.Map position: 19q13.4-19q13.4
 A.Note: highly expressed in colon and pancreatic cancer cells but not in the normal cell
 C.Superfamily: protein-tyrosine-phosphatase, receptor type H; fibronectin type III repeat
 C.Keywords: carcinogenesis; duplication; glycoprotein; phosphoprotein; phosphoric moxed
 F/1-27/Domain: signal sequence #status predicted <SIG>
 F/27-110/Domain: fibronectin type III repeat homology <3FNA>
 F/28-118/Domain: fibronectin type III repeat homology <EXT>
 F/28-118/Domain: fibronectin type III repeat homology <EXT>
 F/116-199/Domain: fibronectin type III repeat homology <3FNB>
 F/205-289/Domain: fibronectin type III repeat homology <3FNC>
 F/296-379/Domain: fibronectin type III repeat homology <3FND>
 F/385-468/Domain: fibronectin type III repeat homology <3FNE>

F/474-558/Domain: fibronectin type III repeat homology <3FNE>
 F/564-658/Domain: fibronectin type III repeat homology <3FNG>
 F/667-737/Domain: fibronectin type III repeat homology <3FNG>
 F/762-778/Domain: fibronectin type III repeat homology <3FNG>
 F/779-1118/Domain: fibronectin type III repeat homology <3FNG>
 F/846-1070/Domain: fibronectin type III repeat homology <3FNG>
 F/35,78,83,107,132,149,172,196,203,286,304,312,329,352,376,383,401,436,439,470,490,558
 F/1024/Active site: Cys (phosphocysteine intermediate) #status predicted
 F/1028/Binding site: substrate phosphate (Arg) #status predicted

Query Match 40.7%; Score 709.5; DB 1; Length 1118;
 Best Local Similarity 48.0%; Pred. No. 7.8e-53;
 Matches 134; Conservative 47; Mismatches 95; Indels 3; Gaps 2;

23 IKINQEGHFKLQADSNVLSKEYELKDVGRNQCIDLLENRGNRYNI 82
 DB IPADPADVHKNRSDNCGPADETQSLVGRNQCIDLLENRGNRYNI 861
 83 RYKLSNVDDPCSDYINASYIPGNFRREYITQGPLFGTKDPFWMVEQNVH 142
 DB 862 RYKLSNVDDPCSDYINASYIPGNFRREYITQGPLFGTKDPFWMVEQNVH 921
 143 QCVKGRVYCDHWPADDSLYYDGLLQMLSESVLEWTEPFKICEBOLA 201
 DB 922 NCMERGVYCDHWPADDSLYYDGLLQMLSESVLEWTEPFKICEBOLA 979
 202 HFTYVTPDHPGVPETTSGLIQFRTVDYINRSPAGPTVVCAGVGRGTGP 261
 DB 980 OFHYQAMPDHPGVPETTSGLIQFRTVDYINRSPAGPTVVCAGVGRGTGP 1039
 262 QQLDSKDSVDYIGAVHDLRLHVMVQTECOVYLLHQCVR 300
 DB 1040 RQLDSKDSVDYIGAVHDLRLHVMVQTECOVYLLHQCVR 1078

Search completed: February 17, 2006, 01:25:38
 Job time: 43 secs

RG Genoscope, Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL: CAE01007048; CAP9510.1; -; Genomic DNA.
 DR Interpro: IPR003961; FN_III.
 DR Interpro: IPR003955; PTPC_motif.
 DR Interpro: IPR003877; TYR_phosphatase.
 DR Interpro: IPR002422; Tyr_PP.
 DR Pfam: PF00041; fn3; 14.
 DR Pfam: PF00102; Y_phosphatase; 1.
 DR PRINTS: PR00700; PRTYPHTASE.
 DR SMART: SM00060; FN3; 14.
 DR SMART: SM00194; PTPC; 1.
 DR SMART: SM00404; PTPC_motif; 1.
 DR PROSITE: PS00853; FN3; 14.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
 KM Hydrolyase.
 FT NON_TER 1 1991
 FT SEQUENCE 1991 AA; 214280 MW; ABECEA629DD27A78 CRC64;
 SQ
 Query Match 67.6%; Score 1178.5; DB 2; Length 1991;
 Best Local Similarity 69.8%; Pred. No. 9,4e-90;
 Matches 213; Conservative 35; Mismatches 46; Indels 9; Gaps 1;
 QY 9 LNLGQKGRKTSCKPIKINQFEGHFMKLDADSNYLLSKYEELKDVGNOSCDIALLPENR 68
 DB 1679 LVYGVRSRRKRGSPVAKGQFOHLDOLADSSVLLSEFEDLDVGRNQADVARPENR 1738
 QY 69 GGRNYNLLPYDARTVKLSNVDDPCSDYINASYIPGNRRERYIVTQPLPGTKDFPK 128
 DB 1739 GGRNYNLLPYDARTVKLSNVDDPCSDYINASYIPGNRRERYIVTQPLPGTKDFPK 1798
 QY 129 NWEQENHNIIVMTVQCCEKGVKCDHWPAODDSLYYGDILLQMLSESVLPWTIREFKI 188
 DB 1799 NWEQENHNIIVMTVQCCEKGVKCDHWPAODDSLYYGDILLQMLSESVLPWTIREFKI 1849
 QY 189 GCEBGLAHRLRHPHYTWPDHGVPTTOSLIQFRTVDYINRSPGAGTVVHCSAGV 248
 DB 1850 GCEBGLAHRLRHPHYTWPDHGVPTTOSLIQFRTVDYINRSPGAGTVVHCSAGV 1909
 QY 249 GRTGFTALRLTIQDLSKDSVDIYGAVHDLRLHRYVMQTECOVYILHOCVRDYLARK 308
 DB 1910 GRTGFTALRLTIQDLSKDSVDIYGAVHDLRLHRYVMQTECOVYILHOCVRDYLARK 1969
 QY 309 LRSBQ 313
 DB 1970 HRGBO 1974
 DB
 RESULT 7
 Q9W6V5 CHICK PRELIMINARY; PRT; 1406 AA.
 ID Q9W6V5
 AC Q9W6V5;
 DT 01-NOV-1999 (TRENDEL, 12, Created)
 DT 01-OCT-2001 (TRENDEL, 18, Last sequence update)
 DT 01-OCT-2003 (TRENDEL, 25, Last annotation update)
 DE Supporting-cell antigen precursor.
 OS Gallus gallus (Chicken).
 CC Birkavoc; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC NCBI_TaxID=9031;
 CC NCBI_TaxID=9031;
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=99296852; PubMed=10366616;
 RA Kruiger R.P., Goodyear R.J., Legan P.K., Warchol M., Raphael Y.,
 RA Cotlanche D.A., Richardson G.P.;

RT "The supporting-cell antigen: a receptor-like protein tyrosine
 RT phosphatase expressed in the sensory epithelia of the inner ear."
 RL J. Neurosci. 19:4815-4827(1999).
 RN (2)
 RP TISSUE=Intestine;
 RC TISSUE=Intestine;
 RA Legan P.K.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 DR EMBL: AJ238216; CAB41885.2; -; mRNA.
 DR HSSP: P18052; IYFO.
 DR Ensembl: ENSGALG0000006392; Gallus gallus.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0016787; F: hydrolyase activity; IEA.
 DR GO: GO:0004725; F: protein tyrosine phosphatase activity; IEA.
 DR GO: GO:0006470; P: protein amino acid dephosphorylation; IEA.
 DR Interpro: IPR003961; FN_III.
 DR Interpro: IPR003877; TYR_phosphatase.
 DR Interpro: IPR002422; Tyr_PP.
 DR Pfam: PF00041; fn3; 9.
 DR Pfam: PF00102; Y_phosphatase; 1.
 DR PRINTS: PR00700; PRTYPHTASE.
 DR SMART: SM00060; FN3; 9.
 DR PROSITE: PS00853; FN3; 10.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
 KM Hydrolyase; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 24
 FT SEQUENCE 1406 AA; 154213 MW; 2D609885C0F367B CRC64;
 SQ
 Query Match 51.0%; Score 889.5; DB 2; Length 1406;
 Best Local Similarity 55.3%; Pred. No. 1.3e-65;
 Matches 162; Conservative 60; Mismatches 64; Indels 7; Gaps 4;
 QY 18 KTSCKPIKINQFEGHFMKLDADSNYLLSKYEELKDVGNOSCDIALLPENRGRNYNLL 77
 DB 1085 KSKIMIKYENESYFKKQDQDSNCGFAEYEEELKSAVQHPKPAALIANRGRNYNLL 1144
 QY 78 PYDARTVKLSNVDDPCS--DYINASYIPGNRRERYIVTQPLPGTKDFPKWAEQNV 135
 DB 1145 PYDISRVKLSN---PCTTDDYINANVMPGYSKXAFIAQGPLPTIIDEFWRMIMWKNI 1201
 QY 136 HNIVMTVQCCEKGVKCDHWPAODDSLYYGDILLQMLSESVLPWTIREFKI GCEBGLD 195
 DB 1202 YSLVMTLCVGRARTCEGYWP-DKQSKSYGDIIVTVVSEVLPWTIRDFVFNADTME 1260
 QY 196 AHELRLRHPHYTWPDHGVPTTOSLIQFRTVDYINRSPGAGTVVHCSAGVGRGTFTI 255
 DB 1261 SH-TVQGHFTSMNPDHGVPTTDLINFRLVHRYSSGNPIDSPILVHCSAGVGRGTFTI 1319
 QY 256 ALDRILQDLSKDSVDIYGAVHDLRLHRYVMQTECOVYILHOCVRDYLARK 308
 DB 1320 ALDRILQDLSKDSVDIYGAVHDLRLHRYVMQTECOVYILHOCVRDYLARK 1372
 DB
 RESULT 8
 PTPRJ HUMAN
 ID PTPRJ HUMAN
 AC Q12913; Q12913; Q8NHM2;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Receptor-type tyrosine-protein phosphatase eta precursor (EC 3.1.3.48)
 DE (Protein-tyrosine phosphatase eta) (R-PTP-eta) (HPTP eta) (Protein-
 DE tyrosine phosphatase receptor type J) (Densily enhanced phosphatase 1)
 DE (DEP-1) (CD148 antigen).
 GN Name=PTPJ; Synonym=DEP1;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Barchontoglires; Primates; Catarrhini; Hominiidae;
 CC Homo

FT VARIANT 214 214 R -> C (in colon cancer; somatic
FT VARIANT 276 276 mutation)
FT VARIANT 276 276 Q -> P (in colon cancer; somatic
FT VARIANT 276 276 mutation; dbSNP:156734).
FT CONFLICT 261 261 G -> D (in Ref. 1).
FT CONFLICT 918 929 YNGKLELUSGR -> LQWENGTSGLP (in Ref. 2).
SQ SEQUENCE 1337 AA; 145927 MW; E6752D52C4B6AF6 CRC64;

Query Match 50.4%; Score 878.5; DB 1; Length 1337;
Best Local Similarity 56.4%; Pred. No. 1e-64;
Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;

QY 18 KTSCEPKINQEGHFKLQADSNYLLSKYEELKDVGNOSCDIALPENRGRKRYNNIL 77
DB 1016 KSKRLIRVNEFAVFKKQADSNCGFAEEYEDKLVGISQKVAELANRGRKRYNNVL 1075
QY 78 PYDARVYLVNVDPCSDYINASYIPGNFRREYIVTQGPLPGLTQDDPFWKWEQVNVN 137
DB 1076 PYDISRVKLS-VQTHSTDDYINANVMGHSKKDFIATQGPLPGLTQDDPFWKWEQVNVN 1134
QY 138 IVMATQCYEGRKVCCHWYPADODSLYYGDLILQMLSESVLPFWTIREFKICGEOLDAN 197
DB 1135 IVMATQCYEGRKVCCHWYPADODSLYYGDLILQMLSESVLPFWTIREFKICGEOLDAN 1193
QY 198 RLIRPHYTYVDPHGVPEPTTOSLIQFVRYVDYINRSPGAGPTVWCHSAGVGTGTFTAL 257
DB 1194 RLIRPHYTYVDPHGVPEPTTOSLIQFVRYVDYINRSPGAGPTVWCHSAGVGTGTFTAL 1252
QY 258 DRILQQLDSKSDYVIGAVHDLRLHRYVHWQTECOYVYLHQCVRDYLARK 308
DB 1253 DRILQQLDSKSDYVIGAVHDLRLHRYVHWQTECOYVYLHQCVRDYLARK 1303

RESULT 9
Q6K302 MOUSE PRELIMINARY; PRT; 1238 AA.

AC 06K302; (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE PPRPT.
CN Name=Prp1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=STS;
RA van Wezel T., Ruijsenkaamp C.A.B., Zanon C., Stassen A.P.M., Vleek C.,
RA Ceikos T., Tripodis N., Groot P.C., Dauwerse H., van Ommen G.J.B.,
RA Demant P.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
DR EMBL; AY039232; AAK98640.1; -. mRNA.
DR HSSP; P18052; IYFO.
DR MGI; MGI:104574; Pcp1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0007507; P:heart development; IMP.
DR GO; GO:0001570; P:vasculogenesis; IMP.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR000387; TYR_PP.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHRTASE.
DR SMART; SM00060; PTPC; 1.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS50853; FN3; 7.
DR PROSITE; PS50853; FN3; 7.

DR PROSITE; PS00183; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KM Hydrolyase; Repeat; Transmembrane.
SQ SEQUENCE 1238 AA; 136772 MW; 0D02F5E8E23C0B2 CRC64;

Query Match 49.8%; Score 869.5; DB 2; Length 1238;
Best Local Similarity 55.7%; Pred. No. 5.4e-64;
Matches 162; Conservative 56; Mismatches 70; Indels 3; Gaps 3;

QY 18 KTSCEPKINQEGHFKLQADSNYLLSKYEELKDVGNOSCDIALPENRGRKRYNNIL 77
DB 917 KSKRLIRVNEFAVFKKQADSNCGFAEEYEDKLVGISQKVAELANRGRKRYNNVL 976
QY 78 PYDARVYLVNVDPCSDYINASYIPGNFRREYIVTQGPLPGLTQDDPFWKWEQVNVN 137
DB 977 PYDISRVKLS-VQTHSTDDYINANVMGHSKKDFIATQGPLPGLTQDDPFWKWEQVNVN 1035
QY 138 IVMATQCYEGRKVCCHWYPADODSLYYGDLILQMLSESVLPFWTIREFKICGEOLDAN 197
DB 1036 IVMATQCYEGRKVCCHWYPADODSLYYGDLILQMLSESVLPFWTIREFKICGEOLDAN 1094
QY 198 RLIRPHYTYVDPHGVPEPTTOSLIQFVRYVDYINRSPGAGPTVWCHSAGVGTGTFTAL 257
DB 1095 RLIRPHYTYVDPHGVPEPTTOSLIQFVRYVDYINRSPGAGPTVWCHSAGVGTGTFTAL 1153
QY 258 DRILQQLDSKSDYVIGAVHDLRLHRYVHWQTECOYVYLHQCVRDYLARK 308
DB 1154 DRILQQLDSKSDYVIGAVHDLRLHRYVHWQTECOYVYLHQCVRDYLARK 1204

RESULT 10
Q61373 MOUSE PRELIMINARY; PRT; 361 AA.

AC 061373;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Protein tyrosine phosphatase (fragment).
CN Name=Prp1; Synonym=PTP-RL9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CS7/B6; Tissue=liver;
RA Higashitsuji H., Arai S., Furutani M., Imamura M., Kaneko Y.,
RA Takenawa T., Nakayama H., Fujita U.,
RT Enhanced expression of multiple protein tyrosine phosphatases in the
RT regenerating mouse liver: Isolation of PTP-RL 10, a novel
RT cytoplasmic-type phosphatase with sequence homology to cytoskeletal
RT protein 4.1.";
RL Oncogene 0:0-0(1995).
DR EMBL; D49393; BAA08386.1; -. mRNA.
DR HSSP; P18052; IYFO.
DR MGI; MGI:104574; Pcp1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0007507; P:heart development; IMP.
DR GO; GO:0001570; P:vasculogenesis; IMP.
DR InterPro; IPR00387; TYR_PP.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHRTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KM Hydrolyase.
SQ NON TER 1 1
SEQUENCE 361 AA; 41726 MW; B514628BD11023AA CRC64;

Query Match 49.8%; Score 868.5; DB 2; Length 361;
 Best Local Similarity 55.7%; Pred. No. 1.3e-64;
 Matches 162; Conservative 56; Mismatches 70; Indels 3; Gaps 3;

18 KTSCEPKINQFEHFMKLOADSNVLSKEYEELKDVGNOSCDIALPENNGKRRNNIL 77
 40 KKSCLIRVENFEAFKQADNSGCPAEYEDLKLIGSLPKYALLENNGKRRNNVL 99
 78 PYDATRYVLSNVDDPCSDYINASYIPGNPFREYITQGPLGTWDFMKVMEQNVN 137
 100 PDISRYVLS-VQTHSTDDYINANVMGHSKQPIATQGPLNTLKDFMFMVMEQNVYA 158
 138 IYWTQCYEKGRKVCCHWPPADQSLYIGDLLOMLSESVLPEWTRREFKICGEBQLDH 197
 159 IYMTKCEGKRTKEEYPSKQ-AQYGDITVANTSEVLPETIRDFVVMNQSSSH 217
 198 RLIRHFHYTWPHGVPETTSLOQFRTVRYNRSFGAPTVHCSAGVGRGTFFIAL 257
 218 PL-RQPHFTSMPHGVPDTDLINFRYIVRYDMKQIPPEPILVHCSAGVGRGTFFIAL 276
 258 DRILQQLDSKDSYDIYGAHDLRLHRYVHWQTECOYVYLHQCVRDYLARK 308
 277 DRLLYQIENENTVDYVGIYDLRMHRLMVQTEQYVFLNQCVLDIIRAK 327

RESULT 11
 062884_RAT PRELIMINARY; PRT; 1216 AA.

AC 062884; RAT PRELIMINARY; PRT; 1216 AA.
 DT 01-NOV-1996 (TRENBERL 01, Created)
 DT 01-NOV-1996 (TRENBERL 01, Last sequence update)
 DT 01-MAR-2004 (TRENBERL 26, Last annotation update)
 DE Vascular protein tyrosine phosphatase 1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_Taxid=10116;
 RX MEDLINE=96375109; PubMed=8781490;
 RA Borges L.G., Seifert R.A., Grant F.J., Hart C.E., Distech C.M., Edelhoff S., Seliger R.A., Lieberman M.A., Lindner V., Fischer E.H., Lok S., Bowen-Pope D.F.;
 RA "Cloning and characterization of rat density-enhanced phosphatase-1, a protein tyrosine phosphatase expressed by vascular cells.";
 RT Circ. Res. 79:570-580(1996).
 RL -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC EMBL: U00790; AB5195.1; mRNA.
 CC HSP: P18052; YPO.
 CC RSD: 3454; PEPY.
 CC GO: GO:0016021; C: integral to membrane; IEA.
 CC GO: GO:0016787; F: hydrolase activity; IEA.
 CC GO: GO:0004725; F: protein tyrosine phosphatase activity; IEA.
 CC GO: GO:0004872; F: receptor activity; IEA.
 CC GO: GO:0004470; P: protein amino acid dephosphorylation; IEA.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR00387; TYR_phosphatase.
 DR InterPro: IPR00242; TYR_PP.
 DR Pfam: PF00041; fn3; 7.
 DR Pfam: PF00102; Y_phosphatase; 1.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR SMART: SM00194; PTPC; 1.
 DR PROSITE: PS00853; FN3; 8.
 DR PROSITE: PS00833; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
 DR Hydrolase; Repeat; Transmembrane.
 SQ SEQUENCE: 1216 AA; 134276 MW; 40613910855391 CRC64;

Query Match 49.8%; Score 868.5; DB 2; Length 1216;
 Best Local Similarity 55.7%; Pred. No. 6.4e-64;
 Matches 162; Conservative 56; Mismatches 70; Indels 3; Gaps 3;

18 KTSCEPKINQFEHFMKLOADSNVLSKEYEELKDVGNOSCDIALPENNGKRRNNIL 77
 40 KKSCLIRVENFEAFKQADNSGCPAEYEDLKLIGSLPKYALLENNGKRRNNVL 99
 78 PYDATRYVLSNVDDPCSDYINASYIPGNPFREYITQGPLGTWDFMKVMEQNVN 137
 100 PDISRYVLS-VQTHSTDDYINANVMGHSKQPIATQGPLNTLKDFMFMVMEQNVYA 158
 138 IYWTQCYEKGRKVCCHWPPADQSLYIGDLLOMLSESVLPEWTRREFKICGEBQLDH 197
 159 IYMTKCEGKRTKEEYPSKQ-AQYGDITVANTSEVLPETIRDFVVMNQSSSH 217
 198 RLIRHFHYTWPHGVPETTSLOQFRTVRYNRSFGAPTVHCSAGVGRGTFFIAL 257
 218 PL-RQPHFTSMPHGVPDTDLINFRYIVRYDMKQIPPEPILVHCSAGVGRGTFFIAL 276
 258 DRILQQLDSKDSYDIYGAHDLRLHRYVHWQTECOYVYLHQCVRDYLARK 308
 277 DRLLYQIENENTVDYVGIYDLRMHRLMVQTEQYVFLNQCVLDIIRAK 327

RESULT 12
 PTPRJ MOUSE STANDARD; PRT; 1238 AA.

AC 064455;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Receptor-type tyrosine-protein phosphatase eta precursor (EC 3.1.3.48)
 DE (Protein-tyrosine phosphatase eta) (R-PTP-eta) (HPTP beta-like tyrosine phosphatase) (protein-tyrosine phosphatase receptor type J)
 DE (Susceptibility to colon cancer-1).
 GN Name=Ptprj; Synonyms=Byp, Soc1;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RX MEDLINE=9610659; PubMed=8549806; DOI=10.1016/0014-5793(95)01415-2;
 RA Kuremochi S., Matsuda S., Matsuda Y., Salton T., Ohnogi M., Yamamoto T.;
 RA "Molecular cloning and characterization of Byp, a murine receptor-type tyrosine phosphatase similar to human DEP-1.";
 RT FEBS Lett. 378:7-14(1996).
 RL -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in every tissue examined.
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Receptor class 3 subfamily.
 CC -1- SIMILARITY: Contains 8 fibronectin type-III domains.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - CC the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC EMBL: D45212; BAA08146.1; mRNA.
 CC PIR: S68700; S68700.
 CC HSP: P18052; YPO.
 CC EMBL: ENSMUSG0000025314; Mus musculus.
 DR MGI: MGI:104574; PEPY.
 DR GO: GO:0005615; C: extracellular space; TAS.
 DR GO: GO:0016021; C: integral to membrane; TAS.


```

Query          18 KTSCPTKINQOEFHFMKLQADSNYLLSKYEELKDVGNQSCDIALPENRGRKRYNNIL 77
Db             917 KKSILIRVENFEAFYFKQADNSQNGFAEYEDLKLIGLSLPTYAEIAENRGRKRYNNVL 976
               | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Query          76 PYDAVTYKLSNVDDPCSDYINASYIGNNFRREYLVTOGFLPOTKODPFMYKWEONVHN 137
Db             977 PYDISVKVLS-VQHSHTDDYINANWFGYHKKDFLATOGLPFTLLKDDFMWYWEKNVYA 1033
               | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Query          138 IYMWTCYKXRYVCHDYPADDSIXYGGLLQWLSSEYLPENWTRFEFKCGEOLDAH 197
Db             1036 IYMWTCYKXRYVCHDYPADDSIXYGGLLQWLSSEYLPENWTRFEFKCGEOLDAH 1094
               | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Query          138 RLIRHRYHYWPHDGVPEPTOSLLOPFRYTRDYINRSAGAFYVWCSNGRGCTETAL 257
Db             1095 PL-RQHFHPSWBDGVPDTLLILNFRYLRDMQKQPPESPLIVWCSNGRGCTETAL 1155
               | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Query          238 DRILQODSKDSVDIYGAHVHDLRLRHVMYQTECOYVTLHOCRDYLRARK 308
Db             1154 DRILYQENIENTVDYGVYIYDRLRHFRHFLWQTEDDYVFLNOCVLDITRAOK 1204
               | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 13
054R5 MOUSE PRELIMINARY; PRT; 1238 AA.
ID 054R5 MOUSE PRELIMINARY; PRT; 1238 AA.
AC 054R5;
DT 13-SEP-2005 (TEMBLrel, 31, Created)
DT 13-SEP-2005 (TEMBLrel, 31, Last sequence update)
DT 13-SEP-2005 (TEMBLrel, 31, Last annotation update).
DE PTPRJ.
DN Name=Ptprj;
NC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BL6/C.
RA van Wesel T., Rutvenkamp C.A.L., Zanon C., Staasen A.P.M., Vlcek C.,
RA Cejka T., Tiripodis N., Groot P.C., Daweise H., van Ommen G.J.B.,
RA Demant P.;
RT Functional cloning identifies Ptpj as the candidate for colon cancer
RT susceptibility QTL Sccl-1.
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
DR EMBL; AY038891; AAK6030.1; -; mRNA.
DR MG1; MG1:104574; Ptpj.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0007507; P:heart development; IMP.
DR GO; GO:0001570; P:vasculogenesis; IMP.
DR KMW Hydroxylase; Repeat; Transmembrane.
SQ SEQUENCE 1238 AA; j36782 MW; 939479EDC8016835 CRC64;

Query Match 49.8%; Score 868.5; DB 2; Length 1238;
Best Local Similarity 55.7%; Pred. No. 6, 5e-64;
Matches 162; Conservative 56; Mismatches 70; Indels 3; Gaps 3;

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QY 198 RLRLHHYVWPHDGVETTSQILQFVATVRYDYNKSPAGPVTWCHSGVGRGTFTAL 257
Db 1095 PLRGHFLSPHBDGVPTDTDLINFRVLVRDMDQIPESPILVCHSGVGRGTFTAL 1154
QY 258 DRLLOQDSKSDVYVACVNDLRLRRHMYQESGVVYVHLCQVADVLRLRX 308
Db 1154 DRLVLYLQENTVNDVQIVYDLDNRHPLMOTEDQVYVPLNCQVADVLRLRX 1204

	RESULT 14	
ID	O8C1W9_MOUSE PRELIMINARY;	PRT; 1238 AA.
AC	O8C1W9;	
DT	01-MAR-2003 (TREMBLrel. 23, Created)	
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)	
DE	Protein tyrosine phosphatase receptor-like protein U.	
OS	Mus musculus (Mouse).	
GN	Name=Puprj;	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;	
OC	Muridae; Murinae; Mus.	
OX	NCBI_Taxid=10090;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=129/SvS1;	
RX	MEDLINE=22064388; PubMed=12089527; DOI=10.1038/hg903;	
RA	Ruiwenhang C.A.L., Van Wezel T., Zanon C., Stassen A.P.M., Vlcek C.,	
RA	Calkos T., Klous A.M., Tripodis N., Petrakis A., Boerigter L.,	
RA	Groot P.C., Lindeman J., Mool W.J., Meijer G.A., Scholten G.,	
RA	Dauvergne H., Peces V., van Zandwijk N., van Ommen G.J.B., Demant P.;	
RT	"Puprj is a candidate for the mouse colon-cancer susceptibility locus	
RT	Sccl and is frequently deleted in human cancers."	
RL	Nat. Genet. 31:295-300(2002).	
DR	EMBL; AY038877; AAN11409.1; ?; Genomic DNA.	
DR	EMBL; AY038861; AAN11409.1; JOINED; Genomic DNA.	
DR	HSSP; PI8052; 1YFO.	
DR	MGI; MGI:104574; Puprj.	
DR	GO; GO:0005615; Cytoextracellular space; TAS.	
DR	GO; GO:0016021; Cellintegral to membrane; TAS.	
DR	GO; GO:0007507; P.heart development; IMP.	
DR	GO; GO:0001570; P.vasculogenesis; IMP.	
DR	InterPro; IPR001361; FN III.	
DR	InterPro; IPR000387; TYR_Phosphatase.	
DR	InterPro; IPR002342; Tyr_PP.	
DR	Pfam; PF00041; fn3; 6.	
DR	PRINTS; PR00700; ERYTHROPHASE.	
DR	SMART; SM00194; FPC3_1.	
DR	PROSITE; PS00583; FNS; 7.	
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.	
DR	PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.	
DR	PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.	
KM	Receptor.	
SQ	SEQUENCE 1238 AA: 136712 MW: DC294E2543995B6C CRC64:	
Query Match	48.9%; Score 853.5; DB 2; Length 1238;	
Best Local Similarity	55.3%; Fred. No. 1.ee-62;	
Matches 161; Conservative	54; Mismatches 73; Indels 3; Gaps 3	
DB	18 KSCPKINOGEGHFKADQDSNYLLSKTEFEELKOVGNSCDIALPPNGKRKNNTL 77	
QY	18 KSKSLRRZNEBEAFKKQQDSDSGCFABEBDALGLSLPKTYAIAIANKRKRNNTV 976	
Db	917 KSKSLRRZNEBEAFKKQQDSDSGCFABEBDALGLSLPKTYAIAIANKRKRNNTV 976	
QY	78 PYDATRVKLSDVDPCSDTIYAISTIRPNFRREYTVYGSLPECTDDPMKMEONVN 137	
Db	977 PYDISIKVLKS-VGHSTIDPIINANTFHEISKDFLATAGFLPLAKDKRWWEKAVTA 1035	
QY	138 IVNVATCEKGRVKCYCHTYPADQDSLITGYDLILQLWLSSYLPEMTIRFKICGEOLDAH 197	
Db	1036 IVNLTCVCEGRKTCEISWYSKO-NQDGIDITAAITSEVLEPTITRDIVVANKNSEH 1094	

QY 196 RLINHEFYVMDHGVETTSLLQFPRATRYKINHBGPGPPIVHCSAGVNGTGLAL 25
Db 1095 PL-RQEFPTSMEDHGVDTTDLINFEYLLVRDMKQIIPSPSLVHCSAGVNGTGLAI 115
QY 258 DRILQQLDSKDSVYIGVANGHDLRLRHVQVQECQYVYLLHQCVRDYLHARK 308
Db 1154 DELVYQIENENTVYVGIYVLDLHNRHRLVQVTEQDQYVFLNQCVDLILRAOK 1204

	RESULT 15
AC	PTD.DROVE
ID	PTFD1.DROVE
AC	P35992; DBENNG; Q8IR87; Q9YWM1;
DT	01-JUN-1994 (Rel.) 29, Created)
DT	13-SEP-2005 (Rel.) 48, Last sequence update)
DT	13-SEP-2005 (Rel.) 48, Last annotation update)
DE	Tyrosine-protein phosphatase 10D precursor (EC 3.1.3.48) [Receptor-
GN	linked protein-Tyrosine phosphatase 10D] (DPR10d).
DN	Name=TP10D; ORFName=CG1817;
OC	Drosophila melanogaster (fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
NCBI	Taxid=7227;
OR	[1]
RN	NCUTEOTIDE SEQUENCE [MENA] (ISOPFORMS LONG AND SHORT).
RP	TISSUE=embryo;
RC	MELINE=92031988; PubMed=1657402; DOI=10.1016/0092-8674(91)90062-4;
EX	Yang X., Seow K.T., Bahri S.M., Oon S.H., Chia W.;
XX	"Two Drosophila receptor-like tyrosine phosphatase genes are expressed
RT	in a subset of developing axons and pioneer neurons in the embryonic
RT	CNS";
RT	Cell 67:661-673(1991).
RL	[2]
RN	NCUTEOTIDE SEQUENCE [MENA] (ISOPFORM SHORT), AND TISSUE SPECIFICITY.
RP	TISSUE=embryo;
RC	MELINE=92031989; PubMed=1657402; DOI=10.1016/0092-8674(91)90063-5;
EX	Ilan S.S., Isoultas P., Zinn K.
XX	"Three receptor-linked protein-tyrosine phosphatases are selectively
RT	expressed on central nervous system axons in the Drosophila embryo.";
RT	Cell 67:675-685(1991).
RL	[3]
RN	NCUTEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP	STRAIN=Berkley;
RC	MELINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
XX	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
XX	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Henderson S.N.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Galle R.F.,
RA	Sutcliffe G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Burdon R.C., Rogers V.-H.C., Blazer R.G., Champé M., Pfeiffer B.D.,
RA	Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA	Abbill U.F., Agapaynt A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA	Ballow R.W., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Bertram B.P., Bhattacharya D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Boutz J., Brockstein P., Brottier P.,
RA	Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA	de Pablos B., Delcher A., Deng Z., Mayes A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA	Dunham K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA	Foster C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,
RA	Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Havens N.L., Harvey D.A., Heiman T.J., Mei M.-H., Ibeagwae J.,
RA	Hoeft D., Houston K.A., Howell T.J., Wei M.-H., Ibeagwae J.,
RA	Italali M., Kalush F., Kapran G.H., Ke Z., Kemison J.A., Ketchum K.A.,
RA	Kamel B.B., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA	Liu X., Maletta B., McIntosh T.C., Moritz C., Morris J., Mozhayeva A.,
RA	Mexlovic G., Milatina N.V., Moscarello C., Murphy D., McPherson D.,
RA	Meunier S.M., Moy N.K., Murphy B., Murphy L., Murry D.M., Nelson D.L.,
RA	Nelson S.M., Nelson K.A., Nixon R., Nusslein-Dhar B., Padob J.M.,
RA	Palatzkio M., Pittman G.S., Pan S., Polard D.R., Puti V., Reese M.G.,
RA	Rehert K., Remington C., Saunders K.D.C., Scheeler P., Shan H.,

RA Shue B.C., Siden-Klamas I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spreding A.C., Stapleton M., Strong R., Sun E.,
 RA Szyrbas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodard T., Holley K.C., Hu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-P., Zaveri J.S., Zhao W., Zhao G., Zhao Q., Zheng U.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of *Drosophila melanogaster*,"
 RA Science 287:2185-2195(2000).
 RA [4]
 RM GENOME REANNOTATION AND ALTERNATIVE SPLICING.
 RP MEDLINE:22426069; PubMed:12537572;
 RX Mera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bertencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RA "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RA systematic review,"
 RA Genome Biol. 3:RESEARCH0063.1-RESEARCH0063.22(2002).
 RA [5]
 RM NCBI/SCITE SEQUENCE (LARGE SCALE MRNA) (ISOFORM LONG).
 RP STRAIN-BERKELEY, TISSUE-Embryo.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Fatfan D., Frise E.,
 RA George R.A., Gonzalez C., Guatin H., Krommiller B., Li P.W., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Paclob J.M., Parasg V., Park S.,
 RA Patel S.E., Phouanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.E.,
 RA Submitted (Feb-2003) to the EMBL/GenBank/DBJ databases.
 RL -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=4;
 CC Name-Long;
 CC IsoId-P35992-1; Sequence=Displayed;
 CC Name-Short;
 CC IsoId-P35992-2; Sequence=VSP_005143, VSP_005144;
 CC Name=1; Synonyms=B;
 CC IsoId-P35992-3; Sequence=VSP_015266;
 CC Note=No experimental confirmation available;
 CC Name=C;
 CC IsoId-P35992-4; Sequence=VSP_015264, VSP_015265;
 CC Note=No experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Selectively expressed in anterior commissure
 CC and its junctions with the longitudinal tracts.
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Receptor class subfamily.
 CC -1- SIMILARITY: Contains 1 tyrosine-protein phosphatase domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL: M80465; AAA28484.1; -; mRNA.
 DR EMBL: M80465.1; -; mRNA.
 DR EMBL: AE003486; AAFA8072.2; -; Genomic DNA.
 DR EMBL: AE003486; AAFA8072.2; -; Genomic DNA.
 DR EMBL: BT004474; AA042638.1; -; mRNA.
 DR EMBL: BT004474; AA042638.1; -; mRNA.
 DR PIR: D41214; D41214.
 DR HSSP: P10566; 11AR.
 DR Ensemble: CG1817; Drosophila melanogaster.
 DR FlyBase: FBgn004370; FlyID.
 DR GO: GO:0004725; P:protein tyrosine phosphatase activity; IDA.
 DR GO: GO:0004770; P:protein amino acid dephosphorylation; IDA.
 DR InterPro: IPR000282; CytoK_receptor_2.

DR InterPro: IPR003961; FN III.
 DR InterPro: IPR003962; FN III subd.
 DR InterPro: IPR000387; Tyr_Posphatase.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00041; fn3; 10.
 DR Pfam: PF00102; X-phosphatase; 1.
 DR PRINTS: PR00014; ENTPH11.
 DR PRINTS: PR00700; RPTPHPHASE.
 DR SMART: SM00060; FN3; 11.
 DR SMART: SM00194; PTPC; 1.
 DR PROSITE: PS50853; FN3; 11.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
 DR Alternative splicing: Glycoprotein; Hydrolase; Protein phosphatase;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 42
 FT CHAIN 43 1631
 FT TOPO DOM 43 1197
 FT TOPO DOM 1198 1218
 FT TRANS MEM 1219 1631
 FT TOPO DOM 43 119
 FT DOMAIN 120 214
 FT DOMAIN 215 308
 FT DOMAIN 309 402
 FT DOMAIN 403 493
 FT DOMAIN 494 580
 FT DOMAIN 581 669
 FT DOMAIN 670 766
 FT DOMAIN 767 861
 FT DOMAIN 862 955
 FT DOMAIN 956 1048
 FT DOMAIN 1049 1190
 FT DOMAIN 1272 1527
 FT ACT_SITE 1468 1468
 FT CARBOHYD 75 75
 FT CARBOHYD 106 106
 FT CARBOHYD 128 128
 FT CARBOHYD 159 159
 FT CARBOHYD 212 212
 FT CARBOHYD 229 229
 FT CARBOHYD 259 259
 FT CARBOHYD 289 289
 FT CARBOHYD 317 317
 FT CARBOHYD 471 471
 FT CARBOHYD 486 486
 FT CARBOHYD 512 512
 FT CARBOHYD 533 533
 FT CARBOHYD 588 588
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 FT CARBOHYD 687 687
 FT CARBOHYD 719 719
 FT CARBOHYD 723 723
 FT CARBOHYD 823 823
 FT CARBOHYD 841 841
 FT CARBOHYD 874 874
 FT CARBOHYD 908 908
 FT CARBOHYD 925 925
 FT CARBOHYD 1001 1001
 FT CARBOHYD 1104 1104
 FT CARBOHYD 1136 1136
 FT CARBOHYD 1195 1195
 FT VASPLIC 1549 1558
 Query Match 48.8%; Score 850.5; DB 1; Length 1631;
 Blast Local Similarity 55.6%; Pred. No. 3,1e-62;
 Matches 160; Conservative 45; Mismatches 76; Indels 7; Gaps 3;
 QY 22 PIKINQEGHMKLQDSDNYLTKVEYELKQVGNOSCDLALPENRKNRYNNIIPYA 81
 DB 1251 PIIKINPHEIRLMSDSDPFRSBEELKAVGRQPCFADLPCKRKNKRFNIIIPYH 1310

Qy 82 TRVGLSNVDDDDPCSDYINASYYIPGNFRREYIVTQGPLGTQKDEPMKRVMEQVNIWV 141
 Db 1311 SHFKIQVDDDESDYINANVYVPGHNSPREFIVTQGPLHSTRDPMKCMESNSRAIVWL 1370
 Qy 142 TQCEKRVKCHVYVAPADSLIYGDLIOMSESVPBWTIEKIC-GEQOLDARLI 200
 Db 1371 TRCEKREKCDQYVNDIVFVFGDIKQIINDSHADWMTFMDLRSSEQ---RIL 1426
 Qy 201 RHFYVWPHDGVPETTQSLIQFRTVNDYINRSPGAGPTVHCSAGVGTGTFIALDRI 260
 Db 1427 RHFFHTWPPPGVNPQTLVRFVRAFRDRIGAE--ORPTVHCSAGVGRSGTFTLDR 1484
 Qy 261 LQQLSDSDYDIYGAVHDLRLHRVHWVQTECOYVYLHQCVRDVLRARK 308
 Db 1485 LQQINTSDYDIFGIYAMRKERVWVQTEQOYICIHQCLLAVLEGEK 1532

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